

STE20_h	MAHLRGFANQHSRV	DPPEELFTKL	DRIGKGSFGEV	YKGI	DNHTK	43																																								
MST3_h	MAHSPVQSGLPQMNLKA	DPEELFTKLEK	IGKGSFGEV	FKGI	DNRTQ	47																																								
STLK2_h	MAHSPVAVQVPQMNNIA	DPEELFTKLEK	ERIGKGSFGEV	FKGI	DNRTQ	47																																								
STLK3_h	TAAPAAPAPAPAAQAVGWPI	CRDAYELQ	EVIGSGATAV	VQAA	LCKPRQ	57																																								
STE20_h	EVVAIKIIDL	EEAEIEDIQ	QEIITVLSQ	CDSPYITR	YFGSYLKSTKL	WIIMEYLG	100																																							
MST3_h	KVVAIKIIDL	EEAEIEDIQ	QEIITVLSQ	CDSPYVTK	YYGSYLKDTKL	WIIMEYLG	104																																							
STLK2_h	QVVAIKIIDL	EEAEIEDIQ	QEIITVLSQ	CDSSYVTK	YYGSYLKSGSKL	WIIMEYLG	104																																							
STLK3_h	ERVAIKRI	NLEKQTSMD	ELLKEIQAM	SQCSHPNVVT	YYTSFVVKDEL	WLV	MKL	LSG	114																																					
STE20_h	GSALDLLKPGP	LEET	YIATILRE	ILKGLDYLHSE	RKI	H	R	D	I	K	A	A	N	V	L	L	148																													
MST3_h	GSALDLLKPGP	LDET	YIATILRE	ILKGLDYLHSE	KKI	H	R	D	I	K	A	A	N	V	L	L	152																													
STLK2_h	GSALDLLKPGP	FDEF	YIATMLKE	ILKGLDYLHSE	KKI	H	R	D	I	K	A	A	N	V	L	L	152																													
STLK3_h	GSMLD	IIKIYIVNR	GEHKN	GVLE	EAI	IATILKE	VLEGLDYLH	R	NGQ	I	H	R	D	L	K	A	G	N	I	L	L	171																								
STLK4_h	-----	-----	KS	GVLD	XST	IATILRE	VLEGL	E	Y	L	H	K	X	G	Q	I	H	R	D	V	K	A	G	N	I	L	X	41																		
STE20_h	SEQGDDV	KLADFGV	A	-----	GQL	T	D	T	Q	I	K	R	N	T	F	V	G	T	P	F	W	M	A	P	E	V	I	K	Q	S	A	-	Y	D	F	K	A	D	I	198						
MST3_h	SEHGEV	KLADFGV	A	-----	GQL	T	D	T	Q	I	K	R	N	T	F	V	G	T	P	F	W	M	A	P	E	V	I	K	Q	S	A	-	Y	D	S	K	A	D	I	202						
STLK2_h	SEQGDDV	KLADFGV	A	-----	GQL	T	D	T	Q	I	K	R	N	T	F	V	G	T	P	F	W	M	A	P	E	V	I	K	Q	S	A	-	Y	D	S	K	A	D	I	202						
STLK3_h	GEDG	SVQ	IADFGV	SA	FL	A	T	G	G	D	V	T	R	N	K	V	-	R	K	T	F	V	G	T	P	C	W	M	A	P	E	V	M	E	Q	V	R	G	Y	D	F	K	A	D	M	227
STLK4_h	GEDG	SVQ	IADFGV	SA	FL	A	T	G	G	D	I	T	R	N	K	V	-	R	K	T	F	V	G	T	P	C	W	M	A	P	E	V	M	E	Q	V	R	G	Y	D	F	K	A	D	I	97

Fig. 1A



STE20_h	RQ--PRSQCLSTLVRPVPVFGELKEKHKQSGGSGVGALEELENAFSLAEE	SCPGISDKLM	405
MST3_h	IPKRPFSCCLSTIISPLFAELKEKSKQACGGNLSIEELRGAIYLAEEA	CPGISDTMV	411
STLK2_h	-----CLSMIITPAFAELKQQDENNASRNQAIIEEL	EKSI AVAA	400
STLK3_h	DY--REASSCAVNLVLRNLSRKEINLDIRFEFTPGRDTADGV	SQELF	468
STLK4_h	-----ISLVRLRNSKKEINLDIRFEFTPGRDTAEGV	SQELISAGLVDGRDL	366
STE20_h	VHLVERVQRF	SHNRNHLTSTR	426
MST3_h	AQLVQRLQRYSL	SGGGTSSH	431
STLK2_h	KKLIEKFQKCS	ADESP	416
STLK3_h	VIVAAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFAQLSVS		516
STLK4_h	VIVAAANLQKIVEEPQSNR	SVTFKLASGVEGSDIPDDGKLGFAQLSIS	414

Fig. 1C

[illegible]

Protein	Sequence	Position
Ste20_h	GSA L D L L K P G P L E E T Y I A T I L R E I L K G L D Y L H S E R K I H R D I K A A N V L L S E Q G D V K L I A	157
T19A5.2_ce	GSA L D L T K S G K L D E S H I A V I L R E I L K G L E Y L H S E R K I H R D I K A A N V L V S E H G D V K V A	171
Pak_sp	GSL T E V V T N N T L S E G Q I A A I C K E T L E G L Q H L H E N G I V H R D I K S D N I L L S L Q G D I K L I T	139
STLK5_h	- - L I C T H F M D G M N E L A I A Y I L Q G V L K A L D Y I I H M G Y V H R S V K A S H I L I S V D G K V Y L S	55

Ste20_h	D F G V A G Q L T D T Q I K R N T F V G T P F - - - - - W M A P E V I K Q S A - - Y D F K A D I W S L G I T A	205
T19A5_2-ce	D F G V A G Q L T E T V K K R I T F V G S P F - - - - - W M A P E L I K Q S S - - Y D Y K A D I W S L G I T A	219
Pak_sp	D F G F C A Q I D S N M T K R T I M V G T P Y - - - - - W M A P E V V T R K E - - Y G F K V D V W S L G I M A	187
STLK5_h	G L R S N L S M I S A G Q R Q R V V H D F P K Y S V K V L P W L S P E V L Q Q N L Q G G Y D A K S D I Y S V G I T A	112

Ste20_h	I E L A K G E P P N S D L H P M R V L F L I P K - N S P P T L E G - Q - - - - -	238
Tt19A5.2_ce	I E L A N G E P P H S D L H P M R V L F L I P K - N P P P V L Q G S Q - - - - -	253
pak_sp	I E M V E G E P P Y L N E N P L R A L Y L I A T I G T P K I S R P E L - - - - -	222
StlK5_h	C E L A N G H V P F K D M P A T Q M L L E K L N - G T V P C L D - T S T I P A E E L T M S P S R S V A N S G L S	167

**Fig. 2A**





ZC504.4\_ce

NIK\_m

ZC1\_h

42Z

ZC3\_h

[illegible]

ZC504.4\_ce

NIK\_m

ZC1\_h

ZC2\_h

ZC3\_h

DDEED	EIKLE	INMLK	KHSHHRN	VATYYGAF	IKKL	PSSTGKH	DQLWL	VMEFCGS	GSITDLVK	116
DDEEEE	ITL	INMLK	KYSHHRN	IATYYGAF	IKKSP	GHD	--	DQLWL	VMEFCGS	ITDLVK
DDEEEE	EIKL	INMLK	KYSHHRN	IATYYGAF	IKKSP	GHD	--	DQLWL	VMEFCGS	ITDLVK
DDEEEE	EIKL	INMLK	KYSHHRN	IATYYGAF	IKKSP	GHD	--	DQLWL	VMEFCGS	ITDLVK
DDEEEE	EIKQ	INMLK	KYSHHRN	IATYYGAF	IKKN	PPGMD	--	DQLWL	VMEFCGS	VTDLIK
DDEEEE	EIKQ	INMLK	KYSHHRN	IATYYGAF	IKKSP	PPGND	--	DQLWL	VMEFCGS	VTDLVK

ZC504.4\_ce

NIK\_m

ZC1\_h

7C2\_h

ZC3\_h

NTKGGSLKE	EWIAYICREILRGL	YHLHQ	SKV	IHRDIKGQNVLL	TD	SAEVKLVDFGVSAQL	176
NTKGNLTKED	WIAIYSREILRGL	AHLH	IHHV	IHRDIKGQNVLL	TENAEVKLVDFGVSAQL		177
NTKGNLTKED	WIAIYSREILRGL	AHLH	IHHV	IHRDIKGQNVLL	TENAEVKLVDFGVSAQL		178
NTKGNLTKED	EWIAYICREILRGL	SHLHQ	HKV	IHRDIKGQNVLL	TENAEVKLVDFGVSAQL		144
NTKGNLTKED	ICIAIYICREILRGL	AHLH	AHKV	IHRDIKGQNVLL	TENAEVKLVDFGVSAQL		144

ZC504.4\_ce

NIK\_m

41Z

zC2\_h

ZC3\_h

DK	TV	GRR	NT	FI	GT	PY	WM	AE	VI	AC	DE	SP	EA	TY	DS	LR	SL	WG	IT	AL	EA	EG	HP	PL	CD	MHP	236
DRT	VG	RR	NT	FI	GT	PY	WM	AE	VI	AC	DE	NP	DA	TY	DR	YR	SL	WG	IT	AL	EA	EG	GP	PL	CD	MHP	237
DRT	VG	RR	NT	FI	GT	PY	WM	AE	VI	AC	DE	NP	DA	TY	DR	YR	SL	WG	IT	AL	EA	EG	GP	PL	CD	MHP	238
DRT	VG	RR	NT	FI	GT	PY	WM	AE	VI	AC	DE	NP	DA	TY	DR	YR	SL	WG	IT	AL	EA	EG	GP	PL	CD	MHP	204
DRT	VG	RR	NT	FI	GT	PY	WM	AE	VI	AC	DE	NP	DA	TY	DR	YR	SL	WG	IT	AL	EA	EG	GP	PL	CD	MHP	204

**Fig. 3A**

**Fig. 3B**



ZC504.4_ce	-----NSGHGAYKGKKIPEIRPGIISL-DDDDSD	623
NIK_m	-----AWSRSDSDEVPRVPVVRTTSRSPVLSRRD	639
ZC1_h	-----PQVPVVRTTSRSPVLSRRD	648
ZC2_h	NSDPTSENPPPLPTRIEKFDRSSWLRQEEDI	635
ZC3_h	NSDPTSEGGPSPNPP-----AWVRPD-NEAPPKVPQRTSS	689
	-----IATA	
	-----LNTSGAGGSRPAQAVR	
ZC504.4_ce	SDNE-----EGNEPLMFKPIVRCPSIFFWFLS	651
NIK_m	QAGQ-----RNSTSSIEPRLLWERVEKLVPRPG	667
ZC1_h	SQAG-----QRNSTSIEPRLLWERVEKLVPRPG	676
ZC2_h	LGSQ-----PIRASNPDLRRTTEPILESP	665
ZC3_h	ARPRSNSAWQIYLQRRRAERGTPKPPPAQPPPPNAS	742
	-----SNPDLRRSDPG-----WERS	
ZC504.4_ce	--ANVIHSVDGSIPLVKHLIWFQNAS	709
NIK_m	--SGSSSGSSNSGSPGSGNPGSQSGSGERFVR	725
ZC1_h	--SGSSSGSSNSGSPGSGNPGSQSGSGERFVR	734
ZC2_h	SSSSSTPSSQPSQSGSQSGSQAGS	725
ZC3_h	--DSVLPASHGHLP-----QAGSLERNRVGV	792
	-----SSKPDSPVLSPGNKAKPDDHRSRPG	
ZC504.4_ce	QPNGFQ-----NSDSR-----SSIQHSFSNRDREK	755
NIK_m	RSCLKPAgev-----DLTAL	777
ZC1_h	RPLKPA-----DLTAL	783
ZC2_h	RPSRPA	785
ZC3_h	RPADFV-----L-----L	837

Fig. 3D

ZC504.4\_ce

NIK\_m

ZC1\_h

ZC2\_h

ZC3\_h

ZC504.4\_ce

NIK\_m

ZC1\_h

422

ZC3\_h

ZC504.4\_ce

VIK\_m

ZC1\_h

ZC2\_h

ZC3\_h

ZC4\_h

ZC504.4\_ce

VIK\_m

ZC1\_h

ZC2\_h

ZC3\_h

ZC4\_h

EGAD	D	S	T	S	G	P	E	D	T	R	A	A	S	S	P	N	L	S	N	G	E	T	E	S	V	K	T	M	I	V	H	D	D	V	E	S	E	P	A	M	T	P	--	--	S	K	E	G	T	L	I	V	--	--	831				
EGAD	E	S	T	S	G	P	E	D	T	R	A	A	S	S	L	N	L	S	N	G	E	T	E	S	V	K	T	M	I	V	H	D	D	V	E	S	E	P	A	M	T	P	--	--	S	K	E	G	T	L	I	V	--	--	837				
E	T	H	D	G	T	V	A	V	S	D	I	P	R	L	I	P	T	G	A	P	G	S	N	E	Q	Y	N	V	G	M	V	G	T	H	G	L	E	T	S	H	A	D	S	F	G	S	I	S	R	E	G	T	L	M	I	R	E	T	845
C	P	A	E	G	S	--	--	--	--	--	--	--	--	--	--	R	D	T	P	G	G	R	D	G	D	T	D	S	V	T	M	V	V	H	D	V	E	I	T	G	T	O	P	P	--	--	Y	G	G	G	T	M	V	I	O	R	T	885	

SSGEKKRSGHSDSNGFAGHINLPDLVQQSHSPAGTPTTEGLGRVSTHSQEMDSGTEYGMGSS 905  
PEEEERNLLHADSNGYT - - - NLPDVVQPSHSPSTENSKGQSPPSKDGSGDYQSRGLVKAPG - 941

[illegible][illegible]

Fig. 3E

ZC504.4\_ce DQM TVLE GQN I L A T I S G R K R R I R V Y Y L S W L R Q K I L R T E G A G S A N T T E K R N G W V N V G D -- 889  
NIK\_m QQM D V L E G L N V L V T I S G K K D K L R V Y Y L S W L R N K I L H N D P E V -- -- -- -- E K K Q G W T T V G D -- 1013  
ZC1\_h QQM D V L E G L N V L V T I S G K K D K L R V Y Y L S W L R N K I L H N D P E V -- -- -- -- E K K Q G W T T V G D -- 1019  
ZC2\_h QQM D V L E G L N V L V T I S G K K N K L R V Y Y L S W L R N R I L H N D P E V -- -- -- -- E K K Q G W I T V G D -- 1077  
ZC3\_h QQM D V L E G L N L L I T I S G K R N K L R V Y Y L S W L R N K I L H N D P E V -- -- -- -- E K K Q G W T T V G D -- 1106  
ZC4\_h R Q L Q V L E P L N L L I T I S G H K N R L R V Y H L T W L R N K I L N N D P E S -- -- -- -- K R R Q E E M L K T E E A C 120

ZC504.4\_ce -- -- -- -- L Q G A I H F K I V R Y E R I K F L V V G L E S S I E I Y A W A P K P Y H K F M S F K S F G S L S H V P L I V 944  
NIK\_m -- -- -- -- L E G C V H Y K V V K Y E R I K F L V I A L K S S V E V Y A W A P K P Y H K F M A F K S F G E L L H K P L L V 1068  
ZC1\_h -- -- -- -- L E G C V H Y K V V K Y E R I K F L V I A L K S S V E V Y A W A P K P Y H K F M A F K S F G E L V H K P L L V 1074  
ZC2\_h -- -- -- -- L E G C I H Y K V V K Y E R I K F L V I A L K N A V E I Y A W A P K P Y H K F M A F K S F A D L Q H K P L L V 1132  
ZC3\_h -- -- -- -- M E G C G H Y R V V K Y E R I K F L V I A L K S S V E V Y A W A P K P Y H K F M A F K S F A D L P H R P L L V 1161  
ZC4\_h K A I D K L T G C E H F S V L Q H E E T T Y I A I A L K S S I H L Y A W A P K S F D E S T A I K V F P T L D H K P V T V 180

ZC504.4\_ce D L T V E D N A R L K V L Y G S T G G F H A I D L D S A A V Y D I Y T P A Q S G Q T T I P H C I V V L P N S N G M Q L L 1004  
NIK\_m D L T V E E G Q R L K V I Y G S C A G F H A V D V D S G S V Y D I Y L P T H I Q C S I K P H A I I I L P N T D G M E L L 1128  
ZC1\_h D L T V E E G Q R L K V I Y G S C A G F H A V D V D S G S V Y D I Y L P T H I Q C S I K P H A I I I L P N T D G M E L L 1134  
ZC2\_h D L T V E E G Q R L K V I F G S H T G F H V I D V D S G N S Y D I Y T P S H I Q G N I T P H A I V I L P K T D G M E M L 1192  
ZC3\_h D L T V E E G Q R L K V I Y G S S A G F H A V D V D S G N S Y D I Y I P V H I Q S Q I T P H A I I I F L P N T D G M E M L 1221  
ZC4\_h D L A I G S E K R L K I F F S S A D G Y H L I D A E S E V M S D V T L P K N P L E I I I P Q N I I L P D C L G I G M M 240

Fig. 3F

ZC504.4\_ce L C Y D N E G V Y V N T Y G R I T K N V V L Q W G E M P S S V A Y I S T G Q I M G W G N K A I E I R S V I D T G H L D G V 1064  
 NIK\_m V C Y E D E G V Y V N T Y G R I T K D V V L Q W G E M P T S V A Y I R S N Q T I M G W G E K A I E I R S V E T G H L D G V 1188  
 ZC1\_h V C Y E D E G V Y V N T Y G R I T K D V V L Q W G E M P T S V A Y I R S N Q T I M G W G E K A I E I R S V E T G H L D G V 1194  
 ZC2\_h V C Y E D E G V Y V N T Y G R I T K D V V L Q W G E M P T S V A Y I H S N Q I M G W G E K A I E I R S V E T G H L D G V 1252  
 ZC3\_h L C Y E D E G V Y V N T Y G R I I K D V V L Q W G E M P T S V A Y I C S N Q I M G W G E K A I E I R S V E T G H L D G V 1281  
 ZC4\_h L T F N A E A L S V E A N E Q L F K K I L E M W K D I P S S I A F E C T D R T T G W G Q K A I E V R S L Q S R V L E S E 300

ZC504.4\_ce F M H K K A Q K L K F L C E R N D K V F F S S A K G G S C Q I Y F M T L N K P G L T N W 1109  
 NIK\_m F M H K R A Q R L K F L C G R N D K V F F S S V R S G G S S Q V Y F M T L G R T S L L S W 1233  
 ZC1\_h F M H K R A Q R L K F L C E R N D K V F F A S V R S G G S S Q V Y F M T L G R T S L L S W 1239  
 ZC2\_h F M H K R A Q R L K F L C E R N D K V F F A S V R S G G S S Q V F F M T L N R N S M M N W 1297  
 ZC3\_h F M H K R A Q R L K F L C E R N D K V F F A S V R S G G S S Q V Y F M T L N R N R I M N W 1326  
 ZC4\_h L K R R S I K K L R F L C T R G D K L F F T T S T L R N H H S R V Y F M T L G K L E E L Q S N Y D V 349

Fig. 3G



**Fig. 4A**



**Fig. 4C**

SULU_ce	L I Q R T K N M V L E L D N F Q Y K K M R K L M Y L D E T E G K E G S E G N G A S D D L D F H G N E A N S I G R A G D S	360
SULU1_h	L I Q R T K D A V R E L D N L Q Y R K M K K I L F	313
SULU3_m	L I Q R T K D A V R E L D N L Q Y R K M K K L L F	309
SULU3_h	L I O R T K D A V R E L D N L O Y R K M K K L L F	103

**Fig. 5A**

SULU\_ce ASSRSASLT SFRSMQSSGGAGLLVSTNTTGAMDNVHGSSGYGNGSSSTTSSARRRRPPIPS 420  
 SULU1\_h ----- QETRNGPPLNES 324  
 SULU3\_m ----- QEAHNGPAVEA 320  
 SULU3\_h ----- QEAHNGPAVEA 114

SULU\_ce QMLSSSTSTSGVGTMP SHG SVGASITAI AVNPTPSPSEPIPTSQPTSKSES S-SILETAHD 479  
 SULU1\_h QED EEDSEHGTS LNREMDSLG SNHSIPSM SVSTGSSQSSSVNSM QEVMD EESSSELVMMHDD 384  
 SULU3\_m QEEEEEQD HGVGR TGT VNSV GSNQSI PSMSISASSSQSSSVNSLPDASDDKS-ELDMMEGD 379  
 SULU3\_h QEEEEEQD HGVGR TGT VNSV GSNQSI PSMSISASSSQSSSVNSLPDVSDDKS-ELDMMEGD 173

SULU\_ce DPLDTSI-----RAPVKDLHMPHRAVKERIA TLQNHK FATLR SQRII 521  
 SULU1\_h ESTINS SS SVVHK KDHVFTRD EAGHGDP RPEPRPTQSVQSQALHYRNRE RFATIKSASLV 444  
 SULU3\_m HTVMSN SS VIHLKPEEENYQE EGDPRTRASDPQSPQVSRHKSHYRNREHFATIR TASLV 439  
 SULU3\_h HTVMSN SS VIHLKPEEENYRE EGDPRTRASDPQSPQVSRHKSHYRNREHFATIR TASLV 233

SULU\_ce NQEQEEYTKENMYEQMSKYKHLRQAHHKELQQFERC ALDREQLRVKMDREL EQLT TTY 581  
 SULU1\_h TRQIHHEHEQENELREQMSGYKKRMRRRQHKKQLIAL ENKLLKAEMDEHRLKLQKEVET HANN S 504  
 SULU3\_m TRQM QEHEQDSELREQMSGYKKRMRRRQHKKQLMTLE NKLLKAEMDEHRLRLDKDLETQRN NF 499  
 SULU3\_h TRQM QEHEQDSELREQMSGYKKRMRRRQHKKQLMTLE NKLLKAEMDEHRLRLDKDLETQRN NF 293

SULU\_ce SKEKMRVRC SQNNELDKRKKDIEDG EKKMKKT KNSQNNQQQMKLYSAQQLKEYKYNKEAQK 641  
 SULU1\_h SIELEKLLAKKQVAIIIEKEAKVAAADEKKFQQQII LAQQKKDL TTFLESQKKQYKICK EKIK 564  
 SULU3\_m AAEMEKLIIKKHQQAAMEKEAKVMANEEKKFQQQHIIQAQQKKELNSFLESQKREYKLRKEQLK 559  
 SULU3\_h AAEMEKLIIKKHQQAAMEKEAKVMSNEEKKFQQQHIIQAQQKKELNSFLESQKREYKLRKEQLK 353

Fig. 5B

SULU\_ce TRLSNM-PRSTYENAMKEVKADLNRVKDAREND FDEKLRRAEL EDEIVRYRRQQQLSNLH 700  
 SULU1\_h EEMNEDHSTPKKEKQERISKHKENLQHTTQAE EEAHLTTQQRLLYYDKNCRFFFKRKIMIKRH 624  
 SULU3\_m EELNENQSTPKKEKQEWLSKQKENIQHFQAE EEAHLTTQQRLLYYDKNCRFFFKRKIMIKRH 619  
 SULU3\_h EELNENQSTPKKEKQEWLSKQKENIQHFQAE EEAHLTTQQRLLYYDKNCRFFFKRKIMIKRH 413

SULU\_ce QLEEQQLDDEVDVNVQERQMDTRHGLLSKQHEMTRDLEIQHNLNELHAMKKRHL ETQHHEAESA 760  
 SULU1\_h EVEEQQNIREEELNKKRRTQKEME HAMLIRHDESTR ELEYRQLHTLQKLRMDLIRLQHQT ETEL 684  
 SULU3\_m NLEQDLVREEELNKKRQTQKDLEHAMLIRQHESMQELEFRHLNTIQKMRCELIRLQHQT ETEL 679  
 SULU3\_h NLEQDLVREEELNKKRQTQKDLEHAMLIRQHESMQELEFRHLNTIQKMRCELIRLQHQT ETEL 473

SULU\_ce SQNEYTQRQQDELRLKKHAMQS RQQPRDLKIQEAQIRKQYRQVVVKTTQTRQFKLYLTQM VQV 820  
 SULU1\_h NQLEYNKKRRERELHRKKHVMGLRQQPKNLKAMEMQIKKKQFQDTCKVVTQKQYKALKNHQLEV 744  
 SULU3\_m NQLEYNKKRRERELRRKKHVM EVRQQPKSLKSKELQIKKKQFQDTCKIQT RQYKALRNHLE T 739  
 SULU3\_h NQLEYNKKRRERELRRKKHVM EVRQQPKSLKSKELQIKKKQFQDTCKIQT RQYKALRNHLE T 533

SULU\_ce VPKDEQKELTSRLKQDQMVKVALLASQYYESQIKKMMVQDKTVKLESWQED EQRVLSEKLEK 880  
 SULU1\_h TPKN EHKTTILKTLKDEQTRKLAIALAEQYEQSINEMMASQALRLDEAQEAECQALLQLQQ 804  
 SULU3\_m TPKN EHKAI 748  
 SULU3\_h TPKSEHKA VLRKLKEEQTRKLAIALAEQYDHSINEMLSTQALRLDEAQEAECQV LKMQ LQQ 593

SULU\_ce ELEELIAYQKKTRATLLEEQIKKERTALEERIGTRRAMLEQKIIIEEEREQMGEMRLKKEQI 940  
 SULU1\_h EMELLNAYQSKIKMQTEAQHERELQKLEQRVSLRRRAHLEQKIIIEEELAA LQKERSERIKNL 864  
 SULU3\_h ELEELLNAYQSKIKMQAEAQHDRELRELQQRVSLRRRAHLEQKIIIEEELM LALQNERTERIRSL 653

Fig. 5C

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*****
720 ICDKERDCLSKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHDLRLRKHEKE 779
721 ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELRLRKHEKE 780

*****
780 REQMQRYNQRMMEQLKVRQQQEKKARLPKIQSDGETRMAMYKKSLHINGAGSASEQREKI 839
781 REQMQRYNQRMIEQLKVRQQQEKKARLPKIQSEGKTRMAMYKKSLHINGGSAAEQREKI 840

*****
840 KQFSQQEKKRQKAERLQQQKKHEHQMRDMVAQCESNMSELQQQNEKCYLLVEHETQKLK 899
841 KQFSQQEKKRQKSERLQQQKKHENQMRDMLAQCESNMSELQQQNEKCHLLVEHETQKLK 900

*****
900 ALDESHNQSLKE 911
901 ALDESHNQNLKE 912

```

Fig. 6C

PAK1_h	MSNNGLDIQDKPPAPP	MRNTSTMIGAGSKDAGTL	NHGS	KPLPPN	PPEEKK	KKKDRFYRSIL	- 59
PAK65_h	MEETQQKSHLELLSA	- - - - -	- - - - -	NHSL	KPLPSV	PPEEKK	KPRHKIISIFS - 40
PAK3_m	-MSDSLNEEKPPAPPLR	- - - - -	MNSNNRDSSALNHSS	KPLPMA	PPEEKN	KKARLSIFPG	54

PAK1_h	PGDK	TNKKKEKERPEIS	LP	PSDFEHTIHVGFD	DA	VTGEFTGM	PEQWARLLQTSNITKS	- - - 115
PAK65_h	GTEK	GSKKKEKERPEIS	PP	PSDFEHTIHVGFD	DT	VTGEFTGM	PEQWARLLQTSNITKL	- - - 96
PAK3_m	GGDK	TNKKKEKERPEIS	LP	PSDFEHTIHVGFD	DA	VTGEFTGI	PEQWARLLQTSNITKL	- - - 110
PAK4_h	- - -	MFRKKKKRPEIS	AP	QN	FQHRVHTS	FD	PK	EGKFVGL
								PPQWQNI
								LDITLRRPK
								PVVDP
								56

PAK1_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 115
PAK65_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 96
PAK3_m	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 110
PAK4_h	SRITRVQLQPMKTVVRGS	AMPVDGYISGLLNDIQKLS	VISSNTLRGRSPT	SRRAQSLGL	116			

PAK1_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 115
PAK65_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 96
PAK3_m	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 110
PAK4_h	LGDEHWATDPDMYLQSPQ	SERTDPHGLYLS	CNGGTPAGHKQMPWPEP	QSPRVLPNGLAAK	176			

PAK1_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 127
PAK65_h	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 108
PAK3_m	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - 122
PAK4_h	AQSLGPAEFQGASQRCLQL	GACLQSSPPGASPP	TGTRNRHGMKA	AKHGS	FEARPQ	SCLVGS	236	

Fig. 7A



PAK1_h	GDELWVVM EYLAGGSLTDVVVTE	TCTC	MDEG	QIAAVCRECLQAL	ESLH	SNQVVIHRDIKSDN	IL	396
PAK65_h	GDELWVVM EYLAGGSLTDVVVTE	TCTC	MDEA	QIAAVCRECLQAL	EF	LHANQVVIHRDIKSDN	VL	357
PAK3_m	GDELWVVM EYLAGGSLTDVVVTE	TCTC	MDVG	QIAAVCRECLQAL	DF	LH	SNQVVIHRDIKSDN	IL
PAK4_h	GDELWVVM EYLAGGSLTDVVVTE	TCTC	MDVG	QIAAVCRECLQAL	DF	LH	SNQVVIHRDIKSDN	IL
PAK5_h	GDELWVVM EYLAGGSLTDVVVTE	TCTC	MDVG	QIAAVCRECLQAL	DF	LH	SNQVVIHRDIKSDN	IL

PAK1_h	LGM	DG	SV	KL	T	D	F	G	F	C	A	Q	I	T	P	E	Q	S	K	R	S	T	M	V	G	T	P	Y	W	M	A	P	E	V	V	T	R	K	A	Y	G	P	K	V	D	I	W	S	L	G	I	M	A	I	E	456					
PAK65_h	LGM	E	G	SV	KL	T	D	F	G	F	C	A	Q	I	T	P	E	Q	S	K	R	S	T	M	V	G	T	P	Y	W	M	A	P	E	V	V	T	R	K	A	Y	G	P	K	V	D	I	W	S	L	G	I	M	A	I	E	417				
PAK3_m	LGM	D	G	SV	KL	T	D	F	G	F	C	A	Q	I	T	P	E	Q	S	K	R	S	T	M	V	G	T	P	Y	W	M	A	P	E	V	V	T	R	K	A	Y	G	P	K	V	D	I	W	S	L	G	I	M	A	I	E	454				
PAK4_h	L	T	D	G	R	V	K	L	S	D	F	G	F	C	A	Q	I	S	K	D	V	P	K	R	K	S	L	V	G	T	P	Y	W	M	A	P	E	V	I	S	R	S	L	Y	A	T	E	V	D	I	W	S	L	G	I	M	V	I	E	593	
PAK5_h	L	T	H	D	G	R	V	K	L	S	D	F	G	F	C	A	Q	V	S	K	E	V	P	R	R	K	S	L	V	G	T	P	Y	W	M	A	P	E	L	I	S	R	L	P	Y	G	P	E	V	D	I	W	S	L	G	I	M	V	I	E	314

PAK1_h	M	I	E	G	E	P	P	Y	L	N	E	N	P	L	R	A	L	Y	L	I	A	T	N	G	T	P	E	L	Q	N	P	E	K	L	S	A	I	F	R	D	F	L	N	R	C	L	E	M	D	V	E	K	R	G	S	A	K	E	L	516	
PAK65_h	M	V	E	G	E	P	P	Y	L	N	E	N	P	L	R	A	L	Y	L	I	A	T	N	G	T	P	E	L	Q	N	P	E	K	L	S	P	I	I	F	R	D	F	L	N	R	C	L	E	M	D	V	E	K	R	G	S	A	K	E	L	477
PAK3_m	M	V	E	G	E	P	P	Y	L	N	E	N	P	L	R	A	L	Y	L	I	A	T	N	G	T	P	E	L	Q	N	P	E	K	L	S	A	V	F	H	D	F	L	N	R	C	L	E	M	D	V	D	R	R	G	S	A	K	E	L	514	
PAK4_h	M	V	D	G	E	P	P	Y	F	S	D	S	P	V	Q	A	M	K	R	L	R	D	S	P	P	P	K	L	K	N	S	H	K	V	S	P	V	L	R	D	F	L	E	R	M	L	V	R	D	P	Q	E	R	A	T	A	Q	E	L	653	
PAK5_h	M	V	D	G	E	P	P	Y	F	N	E	P	P	L	K	A	M	K	M	I	R	D	N	L	P	P	R	L	K	N	L	H	K	V	S	P	S	L	K	G	F	L	D	R	L	L	V	R	D	P	A	Q	R	A	T	A	E	L	374		

PAK1_h	Q	H	Q	F	L	K	I	A	K	P	L	S	S	L	T	P	L	I	A	A	K	E	A	T	K	N	N	H	545
PAK65_h	Q	H	P	F	L	K	L	A	K	P	L	S	S	L	T	P	L	I	M	A	A	K	E	A	M	K	S	N	506
PAK3_m	Q	H	P	F	L	K	L	A	K	P	L	S	S	L	T	P	L	I	I	A	A	K	E	A	I	K	N	S	544
PAK4_h	D	H	P	F	L	Q	T	G	L	P	E	C	L	V	P	L	I	Q	L	Y	R	K	Q	T	S	T	C	681	
PAK5_h	K	H	P	F	L	A	K	A	G	P	P	A	S	I	V	P	L	M	R	Q	N	R	T	R	398				

Fig. 7C

SEQ ID NO: 5 STLK2 human Nterm=1-21 kin=22-274  
Cterm=275-416

MAHSPVAVQVPGMQNNIADPEELFTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEA  
EDEIEDIQQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGSGSALDLLRAGPFDEFQ  
IATMLKEILKGLDYLHSEKKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFV  
GTPFWMAPEVIQQSAYDSKADIWSLGITAIELAKGEPNSDMHPMRVLFLIPKNNPPTLV  
GDFTKSFKEFIDACLNKDPSFRPTAKELLKHKFIVKNSKTSYLTTELIDRFKRWKAEGHS  
DDES DSEGSDSESTSRENNTHPEWSFTTVRKKPDPKKVQNGAEQDLVQTLSCLSMIITPA  
FAELKQQDENNASRNQAIEELEKSIABAEAAACPGITDKMVKKLIEKFQKCSADESP

SEQ ID NO: 6 STLK3 human Nterm=1-31 kin=32-308 Cterm=309-489  
(insert=327-352) tail=490-516

TAAPAPAAPAAPAPAPAPAPAAQAVGWPICRDAYELQEVIGSGATAVVQAALCKPRQERV  
AIKRINLEKCQTSMDLLKEIQAMSQCSPNVVTYYTSFVVKDELWLVMLKLLSGGSMLDI  
IKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIHRDLKAGNILLGEDGSVQIA  
DFGVSAFLATGGDVTRNKVRKTFVGTPCWMAPEVMEQVRGYDFKADMWSFGITAIELATG  
AAPHYKYPKMKVLMMLTLQNDPPTLETGVEDKEMMKYKGSFRKLLSLCLQKDPSKRPTAA  
ELLKCKFFQKAKNREYLIKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWEWSDDM  
DEKSEEGKAASFQEKSRVKEENPEIAVSASTIPEQIQSLSVHDSQGPPNANEDYREASS  
CAVNLVLRRLNSRKELNDIRFEFTPGRDADGVSQELFSAGLVDGHDVVIVAANLQKIVD  
DPKALKTLTFKLASGCDGSEIPDEVKLIGFAQLSVS

SEQ ID NO: 7 STLK4 human Nterm=absent, kin=1-178, Ctail=179-414,  
insert1=198-222, insert2=253-293

KSGVLDXSTIATILREVLEGLEYLHKXGQIHRDVKAGNILXGEDGSVQIADFGVSAFLAT  
GGDITRNKVRKTFVGTPCWMAPEVMEQVRGYDFKADIWSFGITAIELATGAAPHYKYPK  
KVLMLTLQNDPPSLETGVQDKEMMKYKGSFRKMISLCLQKDPEKRPTAAELLRHKFFQK  
AKNKEFLQEKTQRAPTISERAKKVRVPGSSGRLHKTEDGGWEWSDDDEFDEESEEGKAA  
ISQLRSPRVKESISNSELFPPTDPVGTLLQVPEQISAHLPQAPAGQIATQPTQVSLPPTAE  
PAKTAQALSSGSGSQETKIPISLVRLRLNSKKELNDIRFEFTPGRDTAEGVSQELISAGL  
VDGRDLVIVAANLQKIVEEPQSNRSVTFKLASGVEGSDIPDDGKLIGFAQLSIS

SEQ ID NO: 8 STLK5 human Nterm=absent, kin=1-222(lacks N-term),  
Ctail=224-274

LICTHFMGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSN  
LSMISHGQRQRVVHDFPKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSGITACELANGHV  
PFKDMPATQMLLEKLNQTVPCLLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNG  
DSPSHPHYHRTFSPHFHHFVEQCLQRNPDPARPSASTLLNHSFFKQIKRRASEALPELLRPV

TPITNFEQSQSDHSGIFGLVTNLEELEVDDWEF

SEQ ID NO: 13 ZC1 human 1/5/98 Nterm=1-22 kin=23-289

coiled-coil=290-526 pro=527-640 B=641-896 Rab/Rac-BD=897-1239

MANDSPAKSLVDIDLSSLRDPAGIFELVEVVGNGTYGQVYKGRHVKTGQLAAIKVMDVTE  
DEEEEIKLEINMLKKYSHHRNIATYYGAFIKKSPPGHDDQLWLVMFEFCGAGSITDLVKNT  
KGNTLKEDWIAYISREILRGLAHLHIHHVIHRDIKGQNVLLTENA EVKLVD FGVSAQLDR  
TVGRRNTFIGTPYWMAPEVIACDENPDATYDYRSDLWSCGITAIEMAEGAPPLCDMHPMR  
ALFLIPRNPPPRLKSKKWSKKFFSFIEGCLVKNYMQRPSTEQLLKHPFIRDQPNERQVRI  
QLKDHIDRTRKKRGEKDETEYEYSGSEEEEEEVPEQE GEPSSIVNVPGESTLRRDFLR LQ  
QENKERSEALRRQQLLQEQQ LREQEEYKRQLLAERQKR IEQQKEQRRRLEEQQRREREAR  
RQQEREQRRREQE EKRRLEELERRRKEEEEERRRAEEEKRRVEREQEYIRRLQEEEEQRHLE  
VLQQQLLQEQA MLLECRWREMEEHRQAERLQRQLQQEQAYLLSLQHDHRRPHPQHSQQPP  
PPQQERSKPSFHAPEPKAHYEPADRAREVEDRFRKTNHSSPEAQSKQTGRVLEPPVPSRS  
ESFSNGNSESVHPALQRPAEPQVPVRTTSRSPVLSRRDSPLQGGSGQQNSQAGQRNSTSIE  
PRLLWERVEKLVPRPGSGSSSGSSNSGSQPGSHPGSQSGSGERFRVRSSSKSEGSPSQRL  
ENAVKKPEDKKEVFRPLKPADLTALAKELRAVEDVRPPHKVTDYSSSSEESGTTDEEDDD  
VEQEGADESTSGPEDTRAASSLNLSNGETESVKTMIVHDDVESEPA MTPSKEGTLIVRRT  
QSASSTLQKHKSSSSFTPFIDPRLLQISPSSGTTVT SVVGFSCDGM RPEAIRQDPTRKGS  
VVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGVNLLVGTESGLMLLDRSGQGKVYP  
LINRRRFQQMDVLEGLNVLVLTISGKKDKLRVYYLSWLRNKILHNDPEVEKKQGWTTVGD L  
EGCVHYKVVKYERIKFLVIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLVDLTVEE  
GQRLKVIYIGSCAGFHAVD VDSGSVYDIYLP THIQCSIKPHAI IILPNTDGMELLVCYED E  
GVYVNTYGRITKDVVLQWGEMPTSVAYIRSNQTMGWGEKAIEIRSVETGHL DGVFMHKRA  
QRLKFLCERN DKVFFASVRSGGSSQVYFMTLGRTSLLSW

SEQ ID NO: 14 ZC2 human Nterm=missing kin=1-255 coiled-coil=256-442  
pro=443-626 B=627-954 Rab/RacBD=955-1297

AFGEVYEGRHVKTGQLAAIKVMDVTGDEEEEIKQEINMLKKYSHHRNIATYYGAFIKKNP  
PGMDDQLWLVMFEFCGAGSVTDLIKNTKGNTLKEEWIAYICREILRGLSHLHQHKVIHRDI  
KGQNVLLTENA EVKLVD FGVSAQLDR TVGRRNTFIGTPYWMAPEVIACDENPDATYDFKS  
DLWSLGITAIEMAEGAPPLCDMHPMRALFLIPRN PAPRLKSKKWSKKFQSFIESCLVKNH  
SQRPATEQLMKHPFIRDQPNERQVRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEEND  
SGEPSSILNLPRESTLRRDFLR LQLANKERSEALRRQQL EQQQRENEEHKRQLLAERQKR  
IEEQKEQRRRLEEQQRRREKELRKQQEREQRRHYEEQMRREEERRRAEHEQEYKRKQLEE Q  
RQAERLQRQLKQERDYLVS LQHQRQEQR PVEKKPLYHYKEGMSPSEKPAWAKEVEERSRL  
NRQSSPAMPHKVANRISDPNLPPRSESFSISGVQPARTPPMLRPVDPQIPHLVAVKSQGP  
ALTASQSVHEQPTKGLSGFQEALNVTSHRVEMPRQNSDPTSEN PPLPTRIEKFDRSSWLR

QEEDIPPKVPQRTTSSISPALARKNSPGNGSALGPRLGSQPIRASNPDLRRTEPILESPLO  
RTSSGSSSSSSSTPSSQPSQGGSQPGSQAGSSERTRVRANSKSEGSPVLPHEPAKVKEE  
SRDITRPSRPASYKKAIDEDLTALAKELRELRIEETNRPMKKVTDYSSSSSEESSESEEE  
EDGESETHDGTAVSDIPRLIPTGAPGSNEQYNVGMVGTHGLETSHADSFSGSISREGTL  
MIRETSGEKKRSGHSDSNGFAGHINLPDLVQQSHSPAGTPTGLGRVSTHSQEMDSGTEY  
GMGSSTKASFTPFVDPRVYQTSPTDEDEDEEESAAALFTGELLRQEQAALNEARKISVV  
NVNPTNIRPHSDTPEIRKYKKRFNSEILCAALWGVNLLVGTENGLMLLDRSGQGKVYNLI  
NRRRFQQMDVLEGLNVLVLTISGKKNKLRVYYLSWLRNRILHNDPEVEKKQGWITVGDLEG  
CIHYKVVKYERIKFLVIALKNAVEIYAWAPKPYHKFMAFKSFADLQHKPLLVDLTVEEGQ  
RLKVIFGSHTGFHVIDVDSGNSYDIYTPSHIQGNITPHAIVILPKTDGMEMLVCYEDEGV  
YVNTYGRITKDVVLQWGEMPTSVAYIHSNQIMGWGEKAIEIRSVETGHLDGVMHKRAQR  
LKFLCERNDKVFFASVRSGGSSQVFFMTLNRNSMMNW

SEQ ID NO: 15 ZC3 human kin=1-255 coiled-coil=256-476 pro=477-680  
B=681-983 Rab/RacBD =984-1326

AFGEVYEGRHVKTGQLAAIKVMDVTEDEEEEIKQEINMLKKYSHHRNIATYYGAFIKKSP  
PGNDDQLWLVMFCGAGSVTDLVKNTKGNALKEDCIAYICREILRGLAHLHAHKVIHRDI  
KGQNVLLTENAELVDFGVSAQLDRTVGRNRTFIGTPYWMAPVIAACDENPDATYDYRS  
DIWSLGITAIEMAEGAPPLCDMHPMRALFLIPRNPPRLKSKKWSKKFIDFIDTCLIKTY  
LSRPPTQLLKFPFIRDQPTERQVRIQLKDHIDRSRKKRGEKEETEYYSGSEEEEDDSHG  
EEGEPSSIMNVPGESTLRREFLRLQQENKSNSEALKKQQQLQQQQQRDPEAHIKHLLHQR  
QRRIEEQKEERRRVEEQRRREREQRKLQEKEQRRLEDQMALRREEERRQAEREQEYIRH  
RLEEEQRQLEILQQQLLQEQAALLLEYKRKQLEEQRQSERLQRQLQQEHAYLKSLLQQQQQ  
QQLQKQQQQQLLPGDRKPLYHYGRGMNPADKPAWAREVEERTRMNKQQNSPLAKSKPGST  
GPEPPIPQASPGPPGPLSQTTPMQRVPEQEGPHKSLVAHRVPLKPYAAPVPRSQSLQDQ  
PTRNLAAFPASHDPDPAIPAPTATPSARGAVIRQNSDPTSEGGPSPNPPAWVRPDNEAP  
PKVPQRTSSIATALNTSGAGGSRPAQAVRARPRSNSAWQIYLQRRRAERGTPKPPGPPAQP  
PGPPNASSNPDLRRSDPGWERSDSVLPASHGHLPAAGSLERNRVGVSSKPDSSPVLSPGN  
KAKPDDHRSRPGRPADFVLLKERTLDEAPRPPKKAMDYSSSSSEEVESSEDEEEEGEGGPA  
EGSRDTPGGRDGDGTDVSTMVVHDVEEITGTQPPYGGGTMMVVQRTPEEERNLLHADSNY  
TNLPDVVQPSHSPTENSKGQSPPSKDGSGDYQSRGLVKAPGKSSFTMFVDLGIYQPGGSG  
DSIPITALVGGEGTRLQDQLQYDVRKGSVVNVNPTNTRAHSETPEIRKYKKRFNSEILCAA  
LWGVNLLVGTENGLMLLDRSGQGKVYGLIGRRRFQQMDVLEGLNLLITISGKRKNKLRVYY  
LSWLRNKILHNDPEVEKKQGWTTVGDMEGCGHYRVVKYERIKFLVIALKSSVEVYAWAPK  
PYHKFMAFKSFADLPHRPLLVDLTVEEGQRLKVIYGSAGFHAVDSDGNSYDIYIPVHI  
QSQITPHAIIFLPNTDGMEMLLCYEDEGVYVNTYGRIIKDVVLQWGEMPTSVAYICSNQI  
MGWGEKAIEIRSVETGHLDGVMHKRAQRKFLCERNDKVFFASVRSGGSSQVYFMTLNR  
NRIMNW

Title: NUCLEIC ACIDS ENCODING  
PAK5 POLYPEPTIDES AND  
METHODS OF USE THEREOF  
Inventor(s): Gregory PLOWMAN et al.  
DOCKET NO.: 034536-1034

**Fig. 8C**  
28/76



SEQ ID NO: 16 ZC4 human Nterm kin coiled-coil pro B=missing  
Rab/RacBD=1-349

NVNPLYVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLLGTRSNLYLMDRSGKADITKLI  
RRRPFRQIQVLEPLNLLITISGHKNRLRVYHLTWLRNKILNNDPESKRRQEEMLKTEEAC  
KAIDKLTGCEHFSVLQHEETTYIAIALKSSIHLYAWAPKSFDESTAIKVFP TLDHKPVTV  
DLAIGSEKRLKIFFSSADGYHLIDAESEVMSDVTLPKNPLEIIIPQNIILPDCLGIGMM  
LTFNAEALSVEANEQLFKKILEMWKDIPSSIAFECTQRTTGWGQKAIEVRSLQSRVLESE  
LKRRSIKKLRFLCTRGDKLFFTSTLRNHHSRVYFMTLGKLEELQSNDV

SEQ ID NO: 18 KHS2 human Nterm=1-13 kin=14-273 A=274-346  
Pro=347-534 RabBD =535-894

MNPGFDLSRRNPQEDFELIQRIGSGTYGDVYKARNVNTGELAAIKVIKLEPGEDFAVVQQ  
EIIMMKDCKHPNIVAYFGSYLRRDKLWICMEFCGGGSLQDIYHVTGPLSELQIAYVSRET  
LQGLYYLHSGKGMHRDIKGANILLTDNGHVKLADFGVSAQITATIAKRKSFITPYWMA  
EVAVERKGGYNQLCDLWAVGITAEI LAELQPPMFDLHPMRALFLMTKSNFQPPKLKDKM  
KWSNSFHHFVKMALTKNPKKRPTAEKLLQHPFVTQHLTRSLAIELLDKVNNDHSTYHDF  
DDDDPEPLVAVPHRIHSTSRNVREEKTRSEITFGQVKFDPPLRKETEPHHELPDSDGFLD  
SSEIYYTARSNDLQLEYGQGHQGGYFLGANKSLLKSVEEELHQRGHVAHLEDDEGDD  
ESKHSTLKAKIPPLPKPKSIFIPQEMHSTEDENQGTIKRCMSGSPAKPSQVPPRPPP  
PRLPPHKPVALGNGMSSFQLNGERDGS LCQQQNEHRGTNLSRKEKKDVPKPISNGLPPTP  
KVHMGACFSKVFNGCPLKIHCASSWINPDTRDQYLIFGAE EGIYTLNLNELHETSMEQLF  
PRRCTWLYVMNNCLLSISGKASQLYSHNLPGLFDYARQMQLPVAIPAHKLPDRILPRKF  
SVSAKIPETKWCQKCCVVRNPYTGHKYL CGALQTSIVLLEWVEPMQKFMLIKHIDFPIPC  
PLRMFEMLVVPEQEYPLVCVGVSRGRDFNQVRFETVNPNSTSSWFTESDTPQTNVTHVT  
QLERDTILVCLDCCIKIVNLQGR LKSSRKLSSSELT FDFQIESIVCLQDSVLA FWKHGMQG  
RSFRSNEVTQEISDSTRIFRLLGSDRVV VLESRPTDNPTANSNLYILAGHENSY

SEQ ID NO: 22 SULU1 human N=1-21 kin=22-277 A=278-427  
coiled-coil1=428-637 B=638-751 coiled-coil2=752-898

MRKGV LKDPEIDDLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTNEVVAIKKMSYSGK  
QTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQ  
EVEIAAITHGALHGLAYLHSHALHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVG  
TPYWMAPEVILAMDEGQYDGKVDIWSLGITCIELAERKPPLFNMNAMSALYHIAQNDSP  
LQSNEWTDSFRRFVDYCLQKIPQERPTSAELLRHDFVRRDRPLRVLIDLIQRTKDAVREL  
DNLQYRKMKKILFQETRNGPLNESQEDEEDSEHGTS LNREMDSLGSNHSIPSM SVSTGSQ  
SSSVNSMQEVMDESSSELVMMHDESTINSSSSSVVHKKDHVFTRDEAGHGDPRPEPRPTQ  
SVQSQUALHYRNRERFATIKSASLVTRQIHEHEQENELREQMSGYKRMRRQHQQQLIALEN  
KLKAEMDEHRLKLQKEVETHANNSSIELEKLAKKQVAIIEKEAKVAAADEKKFQQQILAQ

QKKDLTTFLESQKKQYKICKKEIKKEEMNEDHSTPKKEKQERISKHKENLQHTQAEAAAHL  
LTQQRLLYYDKNCRFFKRKIMIKRHEVEQQNIREELNKKRTQKEMEAMLI RHDESTRELE  
YRQLHTLQKL RMDLIRLQHQTELENQLEYNKRRERELHRKHVMGLRQOPKNLKAMEMQIK  
KQFQDTCKVQTKQYKALKNHQLEVT PKNEHKTILKTLKDEQTRKLAILAEQYEQSINEMM  
ASQALRLDEAQEAECQALRLQLQQEMELLNAYQSKIKMQTEAQHERELQKLEQRVSLRRA  
HLEQKIEEELAALQKERSERIKNLLERQEREIETFDMESLRMGFGNLVTLDFPKEDYR

SEQ ID NO: 23 SULU3 human Nterm=missing kin partial=1-66 A=67-215  
coiled-coil1=216-425 B=426-539 coiled-coil2=540-786 Ctail=687-786  
IELAERKPPLFNMNAMSALYHIAQNESPTLQSNEWSDYFRNFVDSCLQKIPQDRPTSEEL  
LKHIFVLRERPETVLIDLIQRTKDAVRELDNLQYRKMKKLLFQEAHNGPAVEAQEEEEEQ  
DHGVGRTGTVNSVGSNQSI PSMSISASSQSSSVNSLPDVSDDKSELDMMEGDHTVMSNSS  
VIHLKPEEENYREEGDPRTASDPQSPQVSRHKSHYRNREHFATIRTASLVTRQM QEHE  
QDSELREQMSGYKRMRRQH QKQLMTLENKLKAEMDEHRLRLDKDLETQRNNFAAEMEKL I  
KKHQAAMEKEAKVMSNEEKKFQQHIQAQQKKELNSFLESQKREYKLRKEQLKEELNENQS  
TPKKEKQEWLSKQKENIQHFQAE EEA NLLRRQRQYLELECRRFKRRMLLGRHNLEQDLVR  
EELNKRQTQKDLEHAMLLRQHESMQELEFRHLNTIQKMRC ELIRLQHQTELTNQLEYNKR  
RERELRRKHVMEVRQQPKSLKSKELQIKKQFQDTCKIQTRQYKALRNHLL ETTPKSEHKA  
VLKRLKEEQTRKLAILAEQYDHSINEMLSTQALRLDEAQEAECQVLKMQLQQELELLNAY  
QSKIKMQAEAQHDRELRELEQRVSLRRALLEQKIEEEMLALQNERTERIRSLLE RQAREI  
EAFDSESMRLGFSNMVLSNLSPEAFSHSYPGASGWSHNPTGGPGPHWGHPMGPPQAWGH  
PMQGGPQPWGHPSGPMQGVPRGSSMGVRNSPQALRRRTASGG RTEQGMSRSTSVTSQISNG  
SHMSYT

SEQ ID NO: 24 SULU3 murine Nterm=1-25 kin=26-273 A=274-422  
cc1=423-632 B=633-748 cc2=missing  
MPSTNRAGSLKDPEIAELFFKEDPEKLFTDLREIGHGSFGAVYFARDVRTNEVVAIKKMS  
YSGKQSTEKWQDIIKEVKFLQRIKHPNSIEYKGCYLREHTAWLVMEYCLGSASDLLLEVHK  
KPLQEVEIAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMSPAN  
SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN  
ESPTLQSNMNDSC LQKIPQDRPTSEELLKHMFLRERPETVLIDLIQRTKDAVRELDNLQ  
YRKMKKLLFQEAHNGPAVEAQEEEEEQDHGVGRTGTVNSVGSNQSI PSMSISASSQSSSV  
NSLPDASDDKSELDMMEGDHTVMSNSSVIHLKPEEENYQEEGDPRTASDPQSPQVSRH  
KSHYRNREHFATIRTASLVTRQM QEHEQDSELREQMSGYKRMRRQH QKQLMTLENKLKAE  
MDEHRLRLDKDLETQRNNFAAEMEKL IKKHQAAMEKEAKVMANEEKKFQQHIQAQQKKEL  
NSFLESQKREYKLRKEQLKEELNENQSTPKKEKQEWLSKQKENIQHFQAE EEA NLLRRQR  
QYLELECRRFKRRMLLGRHNLEQDLVREELNKRQTQKDLEHAMLLRQHESMQELEFRHLN  
TIQKMRC ELIRLQHQTELTNQLEYNKRRERELRRKHVMEVRQQPKSLKSKELQIKKQFQD

TCKIQTRQYKALRNHLLLETPKNEHKAI

SEQ ID NO: 26 GEK2 human N=1-33 kin=34-294 A=295-337 B=338-472 215  
coiled-coil1=473-724 215 coiled-coil2=725-912

MAFANFRRLRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGA  
LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLWIMIEFCPPGGAVDA  
IMLELDRGLTEPQIQVVCRQMLEALNFLHSKRIIHRDLKAGNVLMTLEGDIRLADFGVSA  
KNLCTLQKRDSFIGTPYWMAPEVVMCETMKDTPYDYKADIWSLGITLIEMAQIEPPHHEL  
NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLEHPFVSSITSN  
KALRELVAEAKAEVMEEIEDGRDEGEEEDAVIDAASSTLENHTQNSSEVSPPSLNADKPLEE  
SPSTPLAPSQSQDSVNEPCSQPSGDRSLQTTSPPVVAPGNENGLAVPVPLRKS RVPVSM DA  
RIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALET LGGEKLANGSLEPPAQAAPGP  
SKRSDSCSSLCTSESMDYGTNLSTDLSLNKEMGSLSIKDPKLYKKTLKRTRKFVVDGVEV  
SITTSKIISEDEKKDEEMRFLRRQELRELRLQLKEEHRNQTQLSNKHELQLEQMHRFEQ  
EINAKKKFFDTELENLERQQKQQVEKMEQDHAVRRREEARRIRLEQDRDYTRFQEQLKLM  
KKEVKNEVEKLPRQQRKESMKQKMEEHTQKKQLLDRDFVAKQKEDLELAMKRLTTDNRR  
ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELLRKHEKE  
REQMQRYNQRMIEQLKVRQQQEKARLPKIQRSEGKTRMAMYKKS LHINGGGSAAEQREKI  
KQFSQQEEKRQKSERLQQQQKHENQMRDMLAQCESNMSELQQLQNEKCHLLVEHETQKLL  
ALDESHNQN LKE

SEQ ID NO: 29 PAK4 human Rac=1-51 A=52-224 Nterm=225-393  
kin=394-658 Ctail=659-681 residues 13-23

(SAPQNFQHRVH)= Cdc42 /Rac-binding motif

MFRKKKKKRPEISAPQNFQHRVHTSFDPKEGKFVGLPPQWQNILDTLRRPKPVVDPSRIT  
RVQLQPMKTVVRGSAMPVDGYISGLLNDIQKLSVISSNTLRGRSPTSRRRAQSLGLLGDE  
HWATDPD MYLQSPQSERTDPHGLYLSCNGGTPAGHKQMPWPEPQSPRVLPNGLAAKAQSL  
GPAEFQGASQRCLQLGACLQSSPPGASPTGTNRHGMKAAKHGSEEARPQSCLVGSATGR  
PGGEGSPSPKTRESSLKRRFLFRSMFLSTAATAPPSSSKPGPPPQSKPNSSFRPPQKDNPP  
SLVAKAQSLPSDQPVGTFSPLTTSSTSSPQKSLRTAPATGQLPGRSSPAGSPRTWHAQIS  
TSNLYLPQDPTVAKGALAGEDTG VVTHEQFKAALRMVVDQGDPRLLLLDSYVKIGEGSTGI  
VCLAREKHSGRQVAVKMMDLRKQQRRELLFNEVVIMRDYQHFN VVEMYKSYLVGEELWVL  
MEFLQGGALTDIVSQVRLNEEQIATVCEAVLQALAYLHAQGV IHRDIKSDSILLTLDGRV  
KLSDFGFC AQISKDVPKRKSLVGTPYWMAPEVISRSLYATEVDIWSLGIMVIEMVDGEP  
YFSDSPVQAMKRLRDSPPPKLKNSHKVSPVLRDFLERMLVRDPQERATAQELL DHPFLQ  
TGLPECLVPLIQLYRKQTSTC

SEQ ID NO: 30 PAK5 human Rac A=missing Nterm partial=1-114  
kin=115-379 Ctail=380-398

ASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIPQSSSSSSSRPPTRA  
RGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQREPQRVSHEQFRAALQLVVD  
PGDPRSYLDFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQQRRELLFNEVVIMRDY  
QHENVVEMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA  
QGVHRDIKSDSILLTHDGRVKLSDFGFCAQVSKEVPRRKSLVGTPYWMAPELISRLPYG  
PEVDIWSLGIMVIEMVDGEPPYFNEPPLKAMKMIRDNLPPRLKNLHKVSPSLKGFLDRLL  
VRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR

**Fig. 8G**

SEQ ID NO: 1 STLK2 HUMAN

TAACAGCCCACCTCCTAGCCCCGGGCTACGCGCCGCCAGCCCAGTAACCCCACCTTTTGTG  
TGTCCTCCCAGGCCCGGATCGAAAAGCCTGGGAGGGCCGCCGAACCTACCCCCGGAGGGAG  
GAGCCAGTCCGAACCCAAGGCGCCACCGCCGCAGAAGCGGAGCGAGGCAGCATTTCGCCTC  
CATGGCCCACTCGCCGGTGGCTGTCCAAGTGCCTGGGATGCAGAATAACATAGCTGATCC  
AGAAGAACTGTTTACAAAATTAGAGCGCATTGGGAAAGGCTCATTTGGGGAAGTTTTCAA  
AGGAATTGATAACCGTACCCAGCAAGTCGTTGCTATTAAAATCATAGACCTTGAGGAAGC  
CGAAGATGAAATAGAAGACATTCAGCAAGAAATAACTGTCTTGAGTCAATGTGACAGCTC  
ATATGTAACAAAATACTATGGGTCATATTTAAAGGGGTCTAAATTATGGATAATAATGGA  
ATACCTGGGCGGTGGTTCAGCACTGGATCTTCTTCGAGCTGGTCCATTTGATGAGTTCCA  
GATTGCTACCATGCTAAAGGAAATTTTAAAAGGTCTGGACTATCTGCATTTCAGAAAAGAA  
AATTCACCGAGACATAAAAGCTGCCAATGTCTTGCTCTCAGAACAAGGAGATGTTAAACT  
TGCTGATTTTGGAGTTGCTGGTCAGCTGACAGATACACAGATTAAAAGAAATACCTTTGT  
GGGAACTCCATTTTGGATGGCTCCTGAAGTTATTCAACAGTCAGCTTATGACTCAAAAGC  
TGACATTTGGTCATTGGGAATTACTGCTATTGAACTAGCCAAGGGAGAGCCACCTAACTC  
CGATATGCATCCAATGAGAGTTCTGTTTTCTTATTCCCAAAAACAATCCTCCAACCTCTTGT  
TGGAGACTTTACTAAGTCTTTTAAGGAGTTTATTGATGCTTGCCTGAACAAAGATCCATC  
ATTTGCTCCTACAGCAAAAGAACTTCTGAAACACAAATTCATTGTAAAAAATTCAAAGAA  
GACTTCTTATCTGACTGAACTGATAGATCGTTTTAAGAGATGGAAGGCAGAAGGACACAG  
TGATGATGAATCTGATTCCGAGGGCTCTGATTCGGAATCTACCAGCAGGGAAAACAATAC  
TCATCCTGAATGGAGCTTTACCACCGTACGAAAGAAGCCTGATCCAAAGAAAGTACAGAA  
TGGGGCAGAGCAAGATCTTGTGCAAACCTGAGTTGTTTGTCTATGATAATCACACCTGC  
ATTTGCTGAACTTAAACAGCAGGACGAGAATAACGCTAGCAGGAATCAGGCGATTGAAGA  
ACTCGAGAAAAGTATTGCTGTGGCTGAAGCCGCCTGTCCCGGCATCACAGATAAAATGGT  
GAAGAACTAATTGAAAAATTTCAAAGTGTTTCAGCAGACGAATCCCCCTAAGAACTTA  
TTATTGGCTTCTGTTTCATATGGACCCAGAGAGCCCCACCAAACCTACGTCAAGATTAAC  
AATGCTTAACCCATGAGCTCCATGTGCCTTTTGGATCTTTGCAACACTGAAGATTTGGAA  
GAAGCTATTAACTATTTTGTGATGGCGTTTATCATTTTATATTTTGAAAGGATTATTTT  
GTAAGGAATAACTTTTAATACTATAGTTTCACCTGTATTCTAGTAAATGTTGAGACACCG  
TTTTGCTTTTAAGTATCCCTATTTCTTAAGTTACGAGGATGAATACCTTTTACATTTTGA  
TCTTTAGTTGACTCTACAGTCATGAAACATACAGGTCTTTCAAAGTCATTCTCAATATTC  
AGCTTTTGTAAATTATCAAGCTTCAAAAAGCTTTTTTTTAAAAAATAACATGCATATT  
CTAAAAATGACTATTGGTGGGGAGGTGTAAATAAGTCATACCTTCTTAAAACAGAAAATT  
TAAGTAAAGTCTTTTAAATGAAACCTGTAAAAGTATTGACTCTTCTACCAAGTTGGTATG  
ATATTCCAGGCAGCTCAATGATTATCACATTTGAGACCCTGTGTTTGAAGCATTTACAGG  
CAATGTACAGCAACAGAGGTACCTCTTGGTGTATAGTATTTACATTCTCTTTTAGGTAGA  
AGAGGCAATTTTACCCTTATTTTACATGGTTAGAAATTTAAAGCAAGATCATTTACCCAA

GGATAGGTGTTTGGTAATGTTGAAGGAGTTAGTCTGGCTTCATGTTTTACATCTTCAACT  
AAAATCCCATACTATCTGCTTGGATTTGGAGAGCCAAAAAATAAAGCTGATTGTCATGTG  
ATTAAATATCTGATCAACAGGTATGAATATAACTTAAATCAGCATATTTTTGCCATGGTA  
ATAAATTGTCCTATAAACTATTTATATATTTTTGTTCTTCATAATTATCACTAATAAGCA  
TCAGTTTGTGTTTTTAAAGGATATTTAAGTGAGCATTTTCTAGTTCATATGAAAATAA  
CCATAGTACAGGATGATTTCTGTCCACACAAAGGTTAAATTAGATTGCACAGTTAATTTT  
CACTTATATTTATGGTACTATTATGTGGGTGATGCCTTTTTTCTTTTAAGCCCAGTACATA  
TATTATGCCTGCCTAAGTTCTGAACTGGGGCTGTATTTTCAGTAGTTGTAGAATTATTGAT  
ATTTAGTTTTTGATAGCTAATGTTTAAATTGTTTGGATCTGCACAGTTTGGTTTTTGCACAA  
AAGTCATTTAAAAAAATCTGAGTAATTGTCAAATATTTAAAAGAAAGATATTCTTCCTGTA  
AGGAATACAGTTTTTAGTCAAAGTGCCATTACATCCTCTTTTAAATTTACATAATACAG  
ATACTTGAGAAAGTTGTTGTGGTGTTGTATGCCAAGAAAATTCTTTTTATTGGTGCCTAT  
ATTGTAACAATTATTTTAAATGCATTGTATTTTGAAGTAACGGTTCAGTTAAATTTTTCA  
CCTGCTGTGTAAC TGAAACACAATTACAGTTTATAATCATCTGTAGAAGTCTGGAGATAA  
TTTTGCAACTCATGTTATGGGTAAATGAATATTTTTGTAAAAGTAAAAGCAACAAATTT  
ATAAATTGATTATTTGAACTTTACAACACAATTGCATCCCAAATACAAATTGTATTGCT  
TATTCATTATAGCTATTCGTCCTGTAATCTGTTTCTAGGTGAAGCATACTCCAGTGTTTT  
AGGGGTTTTGAAAATAAATATTTAAATTTACAGTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 2 STLK3 HUMAN

GACAGCAGCGCCGGCCCCGGCAGCTCCCGCGGCCCCGGCCCCGGCCCCGGCCCCGGCCCC  
GGCGGCACAGGETGTCGGCTGGCCCATCTGCAGGGACGCGTACGAGCTGCAGGAGGTTAT  
CGGCAGTGGAGCTACTGCTGTGGTTCAGGCAGCCCTATGCAAACCCAGGCAAGAACGTGT  
AGCAATAAAACGGATCAACTTTGAAAAATGCCAGACCAGTATGGATGAACTATTAAAAGA  
AATTCAAGCCATGAGTCAGTGCAGCCATCCCAACGTAGTGACCTATTACACCTCTTTTGT  
GGTCAAAGATGAACTTTGGCTGGTCATGAAATTACTAAGTGGAGGTTCAATGTTGGATAT  
CATAAAATACATTGTCAACCGAGGAGAACACAAGAATGGAGTTCTGGAAGAGGCAATAAT  
AGCAACAATTCTTAAAGAGGTTTTTGAAGGCTTAGACTATCTACACAGAAACGGTCAGAT  
TCACAGGGATTTGAAAGCTGGTAATATTCTTCTGGGTGAGGATGGTTCAGTACAAATAGC  
AGATTTTGGGGTAAGTGC GTTCCTAGCAACAGGGGGTGATGTTACCCGAAATAAAGTAAG  
AAAAACATTCGTTGGCACCCCATGTTGGATGGCTCCTGAAGTCATGGAACAGGTGAGAGG  
CTATGACTTCAAGGCTGACATGTGGAGTTTTTGAATAACTGCCATTGAATTAGCAACAGG  
AGCAGCGCCTTATCACAATATCCTCCCATGAAAGTGTTAATGTTGACTTTGCAAAATGA  
TCCACCCACTTTGGAACAGGGGTAGAGGATAAAGAAATGATGAAAAAGTACGGCAAGTC  
CTTTAGAAAATTACTTTCACTGTGTCTTCAGAAAGATCCTTCCAAAAGGCCACAGCAGC  
AGAACTTTTAAATGCAAATTCTTCCAGAAAGCCAAGAACAGAGAGTACCTGATTGAGAA  
GCTGCTTACAAGAACACCAGACATAGCCCAAAGAGCCAAAAAGGTAAGAAGAGTTCCTGG

Title: NUCLEIC ACIDS ENCODING  
PAK5 POLYPEPTIDES AND  
METHODS OF USE THEREOF  
Inventor(s): Gregory PLOWMAN et al.  
DOCKET NO.: 034536-1034

**Fig. 9B**  
34/76

GTCAAGTGGTCACCTTCATAAAACCGAAGACGGGGACTGGGAGTGGAGTGACGACGAGAT  
 GGATGAGAAGAGCGAAGAAGGGAAAGCAGCTTTTTCTCAGGAAAAGTCACGAAGAGTAA  
 AGAAGAAAATCCAGAGATTGCAGTGAGTGCCAGCACCATCCCCGAACAAATACAGTCCCT  
 CTCTGTGCACGACTCTCAGGGCCCCACCCAATGCTAATGAAGACTACAGAGAAGCTTCTTC  
 TTGTGCCGTGAACCTCGTTTTGAGATTAAGAACTCCAGAAAGGAACTTAATGACATACG  
 ATTTGAGTTTACTCCAGGAAGAGATACAGCAGATGGTGTATCTCAGGAGCTCTTCTCTGC  
 TGGCTTGGTGGATGGTCACGATGTAGTTATAGTGGCTGCTAATTTACAGAAGATTGTAGA  
 TGATCCCAAAGCTTTAAAAACATTGACATTTAAGTTGGCTTCTGGCTGTGATGGGTCGGA  
 GATTCCCTGATGAAGTGAAGCTGATTGGGTTTGCTCAGTTGAGTGTGAGCTGATGTATGTC  
 CCTTGATGTCACCCTGATCTGTCATGCCCCACCGCCACCCCTACTCCCTTCAACCCTCCC  
 TCTTTCTGCCCCATTTCTCCACCCCCCTCACTCCCATTTCTAGCAAAATCAGAAGATTG  
 TGAAGAGGGCCGGCTTCAACAAAATGGGATAAAAAAATAATTTTTTAAACTTTACAACACT  
 CCGAGTTCTGCTTTATTCTCTAGCAATCCACAGTACAAGAACAAAGCAAATGCCACAGCTG  
 CACGACTGTTGCTCATTTTTTCCAAAAGCTATTTAATATTCTTAGCAATCAATTTGGATAT  
 CCCTTAAGTGAAAAGAATCTGAAATACACTCAGGTGGTCTTATTTATTGGCAACAAAAGG  
 AATTTTCTATCCAGAAGCCTATTTCTCCTTTTCAATTGTTGTTATTTCTGTTATAATACTTT  
 AATTGTACATCTGACAATACTGCCTCTTTTTATGTTGTATTTAGAAATTAATATACTTATA  
 AAATTAAGATTTATTAGCCAAACTTGAATTCTAGTTTTAAACTGACTGTGAATTTTATT  
 TTTCATATATTTATGCATTACACACCTTAGCTATAAGAAAAAAGGGTTTTGATTATATG  
 CTTCTTGCAGTTAATCTCGTTATTTAAACAAAAAGTTTTGGGTCTATCTTTGGAGTATTT  
 GTAACCTCTAAATTTTGAAATGACTGAATTAGGAATTTGGATGCTTATTCTTTTAGTCTG  
 TTTGCCTAAAAACCAATTTACAATCTGACTGTCTCTTGGGAGAGGGAGGTGCCTTGCAAA  
 CTTTCACATTAAGAATGTGCCTGAGGCTGCTTTACTCTGGAATAGTCTCAGATCTAAAT  
 TTCCTCTATATAAGGTGGCATAATGTTAAGTTTTGCTTCATTGGACCGTTTAGAATGCTAT  
 GTAAAATGTTGCCATTCTGTTAGATTGCTAACTATATACCCATCTCTGATTTGGCTCTCC  
 TTAAGTGATAGGATTTGTTATTCTAAAGGTGATAAACTTGAAAATATCAGAATCTGAGTT  
 TTACTTGAAATTTTGCAGAATACCCAGGTGGAGTGAAAATTGGAAGGGTTTTGTGCAATG  
 ACTAAAAGGTAAAACGCTGTTAAGGTTCAAGAATCAATACTTTCAACCCAAGTAGCCCTC  
 TGCTTGACTGTATATTATGGAAGTAGTAAACCTTAGGATTTTGAAAATTGGAGTCTAATC  
 TTTCAAGGAGGTGGGCTCCAGGATGGTACCATTGCTCTTTCTAGCTAACCTAGATAT  
 GGCAGCTCTTTAATGTACTTCAAAAAGCAAATATATATTACTAAGGAAAAAAGTTATTT  
 ATAATTGCCTTGTGATAATTGTTAAGGTGTTCTAGAGCCATTTGCATACAATTTAATGTA  
 ATTTCAATCCATTCTATTGTTTACACAACGATTACTCGAAGATGACTGCAAAGGTAAAAG  
 GAAAATAAAAGTGTATTGCACAATGAAAAA

SEQ ID NO: 3 STLK4 HUMAN

CAAAAGTGGAGTCCTAGATGANTCTACCATTGCTACGATACTCCGAGAAGTACTGGAAGG  
 GCTGGAATATCTGCATAAAANTGGACAGATCCACAGAGATGTGAAAGCTGGAACATTCT

Title: NUCLEIC ACIDS ENCODING  
 PAK5 POLYPEPTIDES AND  
 METHODS OF USE THEREOF  
 Inventor(s): Gregory PLOWMAN et al.  
 DOCKET NO.: 034536-1034

**Fig. 9C**  
 35/76

T N T T G G A G A A G A T G G C T C A G T A C A G A T T T C A G A C T T T G G G G T T A G T G C T T T T T T A G C A A C  
 T G G T G G T G A T A T T A C C C G A A A T A A A G T G A G A A A G A C C T T T G T T G G C A C C C C T T G T T G G A T  
 G G C A C C T G A A G T T A T G G A A C A G G T C C G T G G T T A T G A T T T C A A A G C T G A T A T T T G G A G T T T  
 T G G A A T T A C A G C A A T T G A A T T G G C T A C A G G G G C G G C T C C T T A T C A T A A A T A T C C A C C A A T  
 G A A G G T T T T A A T G C T G A C A C T G C A G A A C G A T C C T C C T T C T T T G G A A A C T G G T G T T C A A G A  
 T A A A G A A A T G C T G A A A A A A T A T G G A A A A T C A T T T A G A A A A A T G A T T T C A T T G T G C C T T C A  
 A A A A G A T C C A G A A A A A A G A C C A A C A G C A G C A G A A C T A T T A A G G C A C A A A T T T T T C C A G A A  
 A G C A A A G A A T A A A G A A T T T C T T C A A G A A A A A C A T T G C A G A G A G C A C C A A C C A T T T T C T G A  
 A A G A G C A A A A A A G G T T C G G A G A G T A C C A G G T T C C A G T G G G C G T C T T C A T A A G A C A G A G G A  
 T G G A G G C T G G G A G T G G A G T G A T G A T G A A T T T G A T G A A G A A A G T G A G G A A G G G A A A G C A G C  
 A A T T T C A C A A C T C A G G T C T C C C C G A G T G A A A G A A T C A A T A T C A A A T T C T G A G C T C T T T C C  
 A A C A A C T G A T C C T G T G G G T A C T T T G C T C C A A G T T C C A G A A C A G A T C T C T G C T C A T C T A C C  
 T C A G C C A G C T G G G C A G A T T G C T A C A C A G C C A A C T C A A G T C T C T C T C C C A C C C A C C G C A G A  
 G C C A G C A A A A A C A G C T C A G G C T T T G T C T T C A G G A T C A G G T T C A C A A G A A A C C A A G A T C C C  
 A A T C A G T C T A G T A C T A A G A T T A A G G A A T T C C A A A A A A G A A C T A A A T G A T A T T C G A T T T G A  
 A T T T A C T C C T G G G A G A G A T A C A G C A G A G G G T G T C T C T C A G G A A C T C A T T T C T G C T G G C C T  
 G G T C G A C G G A A G G G A T T T A G T A A T A G T G G C A G C T A A T T T G C A G A A A A T T G T G G A A G A A C C  
 T C A G T C A A A T C G A T C T G T C A C T T T C A A A C T G G C A T C T G G T G T C G A A G G C T C A G A T A T T C C  
 T G A T G A T G G T A A A C T G A T A G G A T T T G C C C A G C T C A G C A T C A G C T A A A C C A C A A C C C T G G A  
 A G A G G C G G C C T A A G G A G A T T C C A C A C A T G C G T A T C T C T G T T G C T T C T A T T G G C C T A A A C C  
 C A C T A C T G C C A A A G A A C C C A G C A A C A A A C C T C C C G G C T A G G A G C T T T A G A A G T C T T T A T G  
 T T C T T C C T G C C A T C A T T C C T C C T T T T C C C A C A G G G A A A G A A A A G T T G G A T C A C T A G T G G C  
 C A G C A T C C C C A G A G T T C C G T T A G T A A A C T T A C T T C A T A T G T C C C C T G T C T T C C T C C A T C T  
 G A G A A G T G G C C C A T G T G C T T C A A G G C C C A G G A G G G A G A T C T G T C A G C T C A T T C T T G C C T T  
 A C T C C A A T G A T G G C C C A G G T G G A A A A G T A G C A G C T G T A T C G G G C T T C C T C A T C C T G C C T G  
 T T C C C C C A C A C C T G C C A G G A T A T G G A C A T C T T G G G A T A T C T C T T T A C C A C T G A A G T A G A A  
 T T G A T T G T T C A G C T G G A G C C C A G A G A A T T T A A T T T A A T G T T T T T C T T T G T A C C T G A T G T  
 G A A T T C T A G C A A C C T T T G T T A G G A A A A A G C A C A G C C T C A G A T G G A G G C A G C C T A A A C T G T  
 G T T C T T G T T T T G T T C A T G G T G T T T C T A A G C G T T T T G C T G A A G C T G C T C T C A G G C A C C C C C  
 T T C T T C A T T G C T C T C T C C A G A A A G G G T T G C T A G C C T T A A C T T C A G C T G G T G C A A A A C A T C  
 T G A C T G T A G C C G A A C T T C A G C C A T C A G A T C C T T C A A A G T G G A A C T T T G G A T T G T T T T T A C  
 A G A C A A C A T C G A G T A A T G G C T T G T A A A T G T G A A T T T T G C C A G A G G T G G T T T T T G A A C A G G  
 A A A A T C A T A A T T C A T A T C A T T G G A G A A G T A T T T A T T T T C A A A T A T C A A A T T G A A G A A A A  
 C T C A A T C C T C C C A T G A A A A T C A G T T C G C C T G G C C T C C A A G T C G T G A G G A A A T G G G T A T G C  
 A A G G C T G A G A T T T C T A C A G C A A T A A A G G A G A C A C A C A C T G G G C C A G A G A G G C C T G C C T T C  
 T G C C T G C T C T C C T G C A C T G A C C C T T T G G A G G G G G T C T C T G T G T G C T G A A G C T A A C T C A A G  
 A T G G A A A G T G A A A C C A C A T G T G C C G T G A C C T T T A G G T T T T A T G A G T A G A C A G T G T T C A T T  
 T G A T T T T C T A C A G A A A T A A T A A A A T T A T T C T T T A G G T T T A A A A A A G A G C A C T C A T A A T G



CAATATGTGAATAATCAGTGAGGTTGATTTTTCTTTTTTCTACCGTTTCATAGTCTTTG  
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AAAAGATACACAAAGATGGGCTGTGGGTCCCTGGAAAGGGGGAGAGTTGCCCTTTACAGA  
ATCACTCGAGCCCTTTCCAGCACTGTTGGTCTGATGAACAAGGTTGTTTTACCTTATTTT  
CTCTTGGAACATATCTGAAAACCTTCCCCACAAATAACTTGTACACACCTTTTGTTCATT  
CTGAGTCTTTAGTTTTAGTCATGGGCTTTCTTCACCTGCTCTAGGTGCAAAGGCATGTTG  
GGAAAGAGATGGATGTTGGGGAGGAAGAGAGGAGATGGATTTTCAGTTGGGAGTTAGGAGG  
AGAGTAGGTGAGATGATCAGACACCGGAGTTCAACGTCCCAGCAGTCTTGGTAAAAGGAG  
GGAGCCTGCTGAGCCAGGAGGGAGAAAAGAAGATTGACCAGCTTGCTAGAAAAATACTTA  
GCTTTTTCTTTTTCTTTTTTTGTGGAGGGGGGACGGAGAGGAACAAGGATGGGGAGGTAGG  
AATGAGGTATAGAAAAGAGATAGCATCTTCTTTGGCACAAGACTAGTGGCTTACCGCTTA  
CCTTAGAGTTTTGTTTTTTTTTTTTCAAACCCATCAAAATCTACTTATTTATGAATCCAA  
GGGGTGGCAGCATCACTCTGTTCTAGCATTCTTTGTGGAGATGGTCTGGTGCCTAGCTGG  
GAGTGAGCAGCAGCCCATCCCCTGTTCACTTTCTCTAGCCCATCATTACCTGTGAACTGC  
AGTGGGGCAGTCATGGCAAATAGAATTGGGCTGGGGTTTCTCCTTCTTTTCAGTTCATTG  
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CATGATGTGTGGTAGACTCCCTTTGCTGGCTTGTGCAGTGATACTGAGAAAATACATGAA  
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ATGCTGATTCAGAGTGCACCTCTTTGACTAGGTCCCAGGATCCCCTTGTCCTTGGAGTAG  
GGACTAACTATAGCACAAAGTAATATGTGCCAATGCTATTTGTGAAATGTTTGGTCTTTC  
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CCTTATGATGTATGCTAGGTTATGGAAGATGTAAAATATTCAACTTTTTCTCCTTTTTT  
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GCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCATGTC  
CCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCC  
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GTGGCCAACTCTGGCCTGAGTGACAGCCTGACCACCAGCACCCCCCGGCCCTCCAACGGT  
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TTCTTCAAGCAGATCAAGCGACGTGCCTCAGAGGCTTTGCCCGAATTGCTTCGTCCTGTG  
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 GTAACAAACCTGGAAGAGCTGGAGGTGGACGATTGGGAGTTCTGAGCCTCTGCAAACCTGT  
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 ATTCCCGCCCTCCTGGGCAGATTGGGTAGAAAGGACATTCTTCCAGGAAAGTTGACTGCT  
 GACTGATTGGGAAAGAAAATCCTGGAGAGATACTTCACTGCTCCAAGGCTTTTGAGACAC  
 AAGGGAATCTCAACAACCAGGGATCAGGAGGGTCCAAAGCCGACATTCCCAGTCCTGTGA  
 GCTCAGGTGACCTCCTCCGCAGAAGAGAGATGCTGCTCTGGCCCTGGGAGCTGAATTCCA  
 AGCCCAGGGTTTGGCTCCTTAAACCCGAGGACCGCCACCTCTTCCCAGTGCTTGCGACCA  
 GCCTCATTCTATTTAACTTTGCTCTCAGATGCCTCAGATGCTATAGGTCAGTGAAAGGGC  
 AAGTAGTAAGCTGCCTGCCTCCCTTCCCTCAGACCTCTCCCTCATAATTCAGAGAAGGG  
 CATTTCTGTCTTTTTTAAGCACAGACTAAGGCTGGAACAGTCCATCCTTATCCCTCTTCTG  
 GCTTGGGCCCTGACACCTAAGTCTTTCCACGGTTTATGTGTGTGCCTCATTCTTTCCC  
 ACCAAGAATCCATCTTAGCGCCTCCTGCCAGCTGCCCTGGTGCTTTCTCCAAGGGCCATC  
 AGTGTCTTGCCTAGCTTGAGGGCTTAAGTCCTTATGCTGTGTTAGTTTCGTTGTCAGAAC  
 AAATTAATAATTTTCAGAGACGCTG

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GAGACCATGGCGAACGACTCTCCCGCGAAAAGTCTGGTGGACATCGACCTCTCCTCCCTG  
 CGGGATCCTGCTGGGATTTTTGAGCTGGTGGAAAGTGGTTGGAAATGGCACCTATGGACAA  
 GTCTATAAGGGTCGACATGTTAAAACGGGTCAGTTGGCAGCCATCAAAGTTATGGATGTC  
 ACTGAGGATGAAGAGGAAGAAATCAAACCTGGAGATAAATATGCTAAAGAAATACTCTCAT  
 CACAGAAACATTGCAACATATTATGGTGCTTTTCATCAAAAAGAGCCCTCCAGGACATGAT  
 GACCAACTCTGGCTTGTTATGGAGTTCTGTGGGGCTGGGTCCATTACAGACCTTGTTGAAG  
 AACACCAAAGGGAAACACACTCAAAGAAGACTGGATCGCTTACATCTCCAGAGAAATCCTG  
 AGGGGACTGGCACATCTTCACATTCATCATGTGATTACCGGGATATCAAGGGCCAGAAT  
 GTGTTGCTGACTGAGAATGCAGAGGTGAAACTTGTTGACTTTGGTGTGAGTGCTCAGCTG  
 GACAGGACTGTGGGGCGGAGAAATACGTTCATAGGCACTCCCTACTGGATGGCTCCTGAG  
 GTCATCGCCTGTGATGAGAACCAGATGCCACCTATGATTACAGAAGTGATCTTTGGTCT  
 TGTGGCATTACAGCCATTGAGATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCATCCA  
 ATGAGAGCACTGTTTCTCATTCCCAGAAACCCTCCTCCCCGGCTGAAGTCAAAAAAATGG  
 TCGAAGAAGTTTTTTAGTTTTATAGAAGGGTGCCTGGTGAAGAATTACATGCAGCGGGCC  
 TCTACAGAGCAGCTTTTGAAACATCCTTTTATAAGGGATCAGCCAAATGAAAGGCAAGTT  
 AGAATCCAGCTTAAGGATCATATAGATCGTACCAGGAAGAAGAGAGGGCGAGAAAGATGAA  
 ACTGAGTATGAGTACAGTGGGAGTGAGGAAGAAGAGAGGAAGTGCTGAACAGGAAGGA  
 GAGCCAAGTTCCATTGTGAACGTGCCTGGTGAAGTCTACTCTTCGCCGAGATTTCTGAGA  
 CTGCAGCAGGAGAACAAGGAACGTTCCGAGGCTCTTCGGAGACAACAGTTACTACAGGAG  
 CAACAGCTCCGGGAGCAGGAAGAATATAAAAGGCAACTGCTGGCAGAGAGACAGAAGCGG

Title: NUCLEIC ACIDS ENCODING  
 PAK5 POLYPEPTIDES AND  
 METHODS OF USE THEREOF  
 Inventor(s): Gregory PLOWMAN et al.  
 DOCKET NO.: 034536-1034

**Fig. 9F**  
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ATTGAGCAGCAGAAAGAACAGAGGCGACGGCTAGAAGAGCAACAAGGAGAGAGCGGGAA  
 GCTAGAAGGCAGCAGGAACGTGAACAGCGAAGGAGAGAAACAAGAAGAAAAGAGGGCGTCTA  
 GAGGAGTTGGAGAGAAGGCGCAAAGAAGAAGAGGAGAGGAGACGGGCAGAAGAAGAAAAG  
 AGGAGAGTTGAAAGAGAACAGGAGTATATCAGGCGACAGCTAGAAGAGGAGCAGCGGCAC  
 TTGGAAGTCCTTCAGCAGCAGCTGCTCCAGGAGCAGGCCATGTTACTGGAGTGCCGATGG  
 CGGGAGATGGAGGAGCACCGGCAGGCAGAGAGGCTCCAGAGGCAGTTGCAACAAGAACAA  
 GCATATCTCCTGTCTCTACAGCATGACCATAGGAGGGCCGCACCCGCAGCACTCGCAGCAG  
 CCGCCACCACCGCAGCAGGAAAGGAGCAAGCCAAGCTTCCATGCTCCCGAGCCCAAAGCC  
 CACTACGAGCCTGCTGACCGAGCGCGAGAGGTGGAAGATAGATTTAGGAAAATAACAC  
 AGCTCCCCCTGAAGCCCAGTCTAAGCAGACAGGCAGAGTATTGGAGCCACCAGTGCCTTCC  
 CGATCAGAGTCTTTTTCCAATGGCAACTCCGAGTCTGTGCATCCCGCCCTGCAGAGACCA  
 GCGGAGCCACAGGTTCTGTGAGAAACAACATCTCGCTCCCTGTTCTGTCCCGTCGAGAT  
 TCCCCACTGCAGGGCAGTGGGCAGCAGAATAGCCAGGCAGGACAGAGAACTCCAACAGT  
 ATTGAGCCCAGGCTTCTGTGGGAGAGAGTGGAGAAGCTGGTGCCCAGACCTGGCAGTGGC  
 AGCTCCTCAGGGTCCAGCAACTCAGGATCCCAGCCCGGGTCTCACCTGGGTCTCAGAGT  
 GGCTCCGGGGAACGCTTCAGAGTGAGATCATCATCAAGTCTGAAGGCTCTCCATCTCAG  
 CGCCTGGAAAATGCAGTGAAAAAACCTGAAGATAAAAAGGAAGTTTTTCAGACCCCTCAAG  
 CCTGCTGATCTGACCGCACTGGCCAAAGAGCTTCGAGCAGTGGAAGATGTACGGCCACCT  
 CACAAAGTAACGGACTACTCCTCATCCAGTGAGGAGTCGGGGACGACGGATGAGGAGGAC  
 GACGATGTGGAGCAGGAAGGGGCTGACGAGTCCACCTCAGGACCAGAGGACACCAGAGCA  
 GCGTCATCTCTGAATTTGAGCAATGGTGAAACGGAATCTGTGAAAACCATGATTGTCCAT  
 GATGATGTAGAAAGTGAGCCGGCCATGACCCCATCCAAGGAGGGCACTCTAATCGTCCGC  
 CGGACTCAGTCCGCTAGTAGCACACTCCAGAAACACAAATCTTCCTCCTCTTTACACCT  
 TTTATAGACCCAGATTACTACAGATTTCTCCATCTAGCGGAACAACAGTGACATCTGTG  
 GTGGGATTTTCTGTGATGGGATGAGACCAGAAGCCATAAGGCAAGATCCTACCCGGAAA  
 GGCTCAGTGGTCAATGTGAATCCTACCAACACTAGGCCACAGAGTGACACCCCGGAGATT  
 CGTAAATACAAGAAGAGGTTTAACTCTGAGATTCTGTGTGCTGCCTTATGGGGAGTGAAT  
 TTGCTAGTGGGTACAGAGAGTGGCCTGATGCTGCTGGACAGAAGTGGCCAAGGGAAGGTC  
 TATCCTCTTATCAACCGAAGACGATTTCAACAAATGGACGTACTTGAGGGCTTGAATGTC  
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 AATAAAATACTTCACAATGATCCAGAAGTTGAGAAGAAGCAGGGATGGACAACCGTAGGG  
 GATTTGGAAGGATGTGTACATTATAAAGTTGTAAATATGAAAGAATCAAATTTCTGGTG  
 ATTGCTTTGAAGAGTTCTGTGGAAGTCTATGCGTGGGCACCAAAGCCATATCACAAATTT  
 ATGGCCTTTAAGTCATTTGGAGAATTGGTACATAAGCCATTACTGGTGGATCTCACTGTT  
 GAGGAAGGCCAGAGGTTGAAAGTGATCTATGGATCCTGTGCTGGATTCCATGCTGTTGAT  
 GTGGATTCAGGATCAGTCTATGACATTTATCTACCAACACATATCCAGTGTAGCATCAAA  
 CCCCATGCAATCATCATCCTCCCCAATACAGATGGAATGGAGCTTCTGGTGTGCTATGAA  
 GATGAGGGGGTTTATGTAAACACATATGGAAGGATCACCAAGGATGTAGTTCTACAGTGG

GGAGAGATGCCTACATCAGTAGCATATATTTCGATCCAATCAGACAATGGGCTGGGGAGAG  
AAGGCCATAGAGATCCGATCTGTGGAACTGGTCACTTGGATGGTGTGTTTCATGCACAAA  
AGGGCTCAAAGACTAAAATTCTTGTGTGAACGCAATGACAAGGTGTTCTTTGCCTCTGTT  
CGGTCTGGTGGCAGCAGTCAGGTTTATTTTCATGACCTTAGGCAGGACTTCTCTTCTGAGC  
TGGTAGAAGCAGTGTGATCCAGGGATTACTGGCCTCCAGAGTCTTCAAGATCCTGAGAAC  
TTGGAATTCCTTGTAAC

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GCTTTCGGGGAGGTCTATGAGGGTCGTCATGTCAAAACGGGGCCAGCTTGCAGCCATCAAG  
GTTATGGATGTCACAGGGGATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAG  
AAATATTCTCATCACCGGAATATTGCTACATACTATGGTGTCTTTTATCAAAAAGAACCCA  
CCAGGCATGGATGACCAACTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACC  
GACCTGATCAAGAACACAAAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGC  
AGGGAAATCTTACGGGGGCTGAGTCACCTGCACCAGCATAAAGTGATTTCATCGAGATATT  
AAAGGGCAAAATGTCTTGCTGACTGAAAATGCAGAAGTTAACTAGTGGACTTTGGAGTC  
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ATGGCACCAGAAGTTATTGCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGT  
GACTTGTGGTCTTTGGGTATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGT  
GACATGCACCCCATGAGAGCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAG  
TCTAAGAAGTGGTCAAAAAAATTCCAGTCATTTATTGAGAGCTGCTTGGTAAAGAATCAC  
AGCCAGCGACCAGCAACAGAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAAT  
GAGCGACAGGTCCGCATTCAACTCAAGGACCATATTGATAGAACAAGAAAGAGGAGGAGAATGAC  
GAAAAAGATGAGACAGAGTATGAGTACAGTGGAAAGTGAAGGAAGAAGAGGAGGAGAATGAC  
TCAGGAGAGCCCAGCTCCATCCTGAATCTGCCAAGGGAGTCGACGCTGCGGAGGGACTTT  
CTGAGGCTGCAGCTGGCCAACAAGGAGCGTTCTGAGGCCCTACGGAGGCAGCAGCTGGAG  
CAGCAGCAGCGGGAGAATGAGGAGCACAAGCGGCAGCTGCTGGCCGAGCGTCAGAAGCGC  
ATCGAGGAGCAGAAAGAGCAGAGGCGGCGGCTGGAGGAGCAACAAAGGCGAGAGAAGGAG  
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GGAATGAGTCCTAGTGAGAAGCCAGCATGGGCCAAGGAGGTAGAAGAACGGTCAAGGCTC  
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ATGCTCAGACCAGTCGATCCCCAGATCCCACATCTGGTAGCTGTAAAATCCCAGGGACCT  
GCCTTGACCGCCTCCCAGTCAGTGCACGAGCAGCCCACAAAGGGCCTCTCTGGGTTTCAG  
GAGGCTCTGAACGTGACCTCCCACCGCGTGGAGATGCCACGCCAGAACTCAGATCCCACC  
TCGGAAAATCCTCCTCTCCCCACTCGCATTGAAAAGTTTGACCGAAGCTCTTGGTTACGA

Title: NUCLEIC ACIDS ENCODING  
PAK5 POLYPEPTIDES AND  
METHODS OF USE THEREOF  
Inventor(s): Gregory PLOWMAN et al.  
DOCKET NO.: 034536-1034

**Fig. 9H**  
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CAGGAAGAAGACATTCCACCAAAGGTGCCTCAAAGAACAACCTTCTATATCCCCAGCATT  
 GCCAGAAAGAATTCTCCTGGGAATGGTAGTGCTCTGGGACCCAGACTAGGATCTCAACCC  
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 AGGACCAGCAGTGGCAGTTCCTCCAGCTCCAGCACCCCTAGCTCCCAGCCCAGCTCCCAA  
 GGAGGCTCCCAGCCTGGATCACAAGCAGGATCCAGTGAACGCACCAGAGTTCGAGCCAA  
 AGTAAGTCAGAAGGATCACCTGTGCTCCCCCATGAGCCTGCCAAGGTGAAACCAGAAGAA  
 TCCAGGGACATTACCCGGGCCAGTCGACCAGCTAGCTACAAAAAAGCTATAGATGAGGAT  
 CTGACGGCATTAGCCAAAGAACTAAGAGAACTCCGGATTGAAGAAACAAACCGCCCAATG  
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 GAAGATGGAGAGAGCGAGACCCATGATGGGACAGTGGCTGTCAGCGACATACCCAGACTG  
 ATACCAACAGGAGCTCCAGGCAGCAACGAGCAGTACAATGTGGGAATGGTGGGGACGCAT  
 GGGCTGGAGACCTCTCATGCGGACAGTTTCAGCGGCAGTATTTCAAGAGAAGGAACCTTG  
 ATGATTAGAGAGACGTCTGGAGAGAAGAAGCGATCTGGCCACAGTGACAGCAATGGCTTT  
 GCTGGCCACATCAACCTCCCTGACCTGGTGCAGCAGAGCCATTCTCCAGCTGGAACCCCG  
 ACTGAGGGACTGGGGCGCGTCTCAACCCATTCCCAGGAGATGGACTCTGGGACTGAATAT  
 GGCATGGGGAGCAGCACCAAAGCCTCCTTCACCCCTTTGTGGACCCAGAGTATACAG  
 ACGTCTCCCACTGATGAAGATGAAGAGGATGAGGAATCATCAGCCGCAGCTCTGTTTACT  
 GGCGAACTTCTTAGGCAAGAACAGGCCAACTCAATGAAGCAAGAAAGATTTTCGGTGGTA  
 AATGTAAACCCAACCAACATTTCGGCCTCATAGCGACACACCAGAAATCAGAAAATACAAG  
 AAACGATTCAACTCAGAAATACTTTGTGCAGCTCTGTGGGGTGTAACCTTCTGGTGGGG  
 ACTGAAAATGGCCTGATGCTTTTTGGACCGAAGTGGGCAAGGCAAAGTCTATAATCTGATC  
 AACCGGAGGCGATTTTCAGCAGATGGATGTGCTAGAGGGACTGAATGTCCTTGTGACAATT  
 TCAGGAAAGAAGAATAAGCTACGAGTTTACTATCTTTTCATGGTTAAGAAACAGAATACTA  
 CATAATGACCCAGAAGTAGAAAAGAAACAAGGCTGGATCACTGTTGGGGACTTGGAAGGC  
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 AATGCTGTGGAAATATATGCTTGGGCTCCTAAACCGTATCATAAATTCATGGCATTTAAG  
 TCTTTTGCAGATCTCCAGCACAAAGCCTCTGCTAGTTGATCTCACGGTAGAAGAAGGTCAA  
 AGATTAAAGGTTATTTTTGGTTACACACTGGTTTCCATGTAATTGATGTTGATTCAGGA  
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 GTCATCTTGCCTAAAACAGATGGAATGGAAATGCTTGTGTTGCTATGAGGATGAGGGGGTG  
 TATGTAAACACCTATGGCCGGATAACTAAGGATGTGGTGGCTCCAATGGGGAGAAATGCC  
 ACGTCTGTGGCCTACATTCAATCCAATCAGATAATGGGCTGGGGCGAGAAAGCTATTGAG  
 ATCCGGTCAGTGGAAACAGGACATTTGGATGGAGTATTTATGCATAAGCGAGCTCAAAGG  
 TTAAGTTTCTATGTGAAAGAAATGATAAGGTATTTTTTGCATCCGTGCGATCTGGAGGA  
 AGTAGCCAAGTGTTTTTTCATGACCCTCAACAGAAATTCATGATACTGGTAACAGAAG  
 AGCACTTGGCACTTATCTTCATGGCGTTATTTCTAATTTAAAGAACATAACTCATGTGG  
 ACTTATGCCAGTCTAGAGGCAGAATCAGAAGGCTTGGTTGAACATATCGCTTTCCCTTTT  
 TCCTCTCCCTCCGCCCCCTCCAGTACAGTCCATCT

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**Fig. 9 I**  
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SEQ ID NO: 11 ZC3 HUMAN

GCATTTGGGGAGGTGTATGAGGGTCTGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAG  
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CCGGGAAACGATGACCAGCTCTGGCTGGTGTATGGAGTTCTGTGGTGCTGGTTTCAGTGACT  
GACCTGGTAAAGAACAACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGC  
AGGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCCACAAGGTGATCCATCGAGACATC  
AAGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTG  
AGTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGG  
ATGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGT  
GATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCTCTGTGT  
GACATGCACCCCATGCGAGCCCTCTTCCTCATTCTCGGAACCTCCGCCCAGGCTCAAG  
TCCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTAC  
CTGAGCCGCCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACG  
GAGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGT  
GAGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGA  
GAGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAG  
TTTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAACAGCAGCAGCAG  
CTGCAGCAGCAGCAGCAGCAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGG  
CAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCTGGAGGAGCAACAGCGGCGG  
GAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAG  
GCTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCTGCAC  
AGGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAG  
GCCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTC  
CAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAG  
CAGCAGCTTCAGAAACAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTAC  
CATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCCGAGAGGTAGAAGAG  
AGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCAG  
GGGCCTGAGCCCCCATCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCAGACT  
CCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAAGAGCCTGGTGGCACAC  
CGGGTCCCACTGAAGCCATATGCAGCACTGTACCCCGATCCCACTCCCTGCAGGACCAG  
CCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCTGCCATCCCCGCA  
CCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACTCT  
GAAGGACCTGGCCCCAGCCCGAATCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCA  
CCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGA  
GGGTCCCGGCCAGCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATC  
TATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCC  
CCTGGCCCCGCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCTGGCTGGGAA

Title: NUCLEIC ACIDS ENCODING  
PAK5 POLYPEPTIDES AND  
METHODS OF USE THEREOF  
Inventor(s): Gregory PLOWMAN et al.  
DOCKET NO.: 034536-1034

**Fig. 9J**  
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CGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAG  
 CGGAACCGCGTGAGGTCTCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAAT  
 AAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTG  
 AAAGAGCGGACTCTGGACGAGGCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCG  
 TCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCCGAAGGCCGGCCAGCA  
 GAGGGGAGCAGAGATACCCCTGGGGGCGCGATGGGGATACAGACAGCGTCAGCACCATG  
 GTGGTCCACGACGTGAGGAGATCACCGGGACCCAGCCCCCATAACGGGGGCGGCACCATG  
 GTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTAC  
 ACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAA  
 AGCCCCACCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCT  
 GGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGG  
 GACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGCACTCGGCTCGACCAGCTGCAG  
 TACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCACAGT  
 GAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCC  
 CTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGT  
 GGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTG  
 GAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAACTGCGGGTGTATTAC  
 TTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGC  
 TGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTTGTGAAATACGAGCGG  
 ATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGCCCCCAA  
 CCCTACCACAAATTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCACCGCCCTCTGCTG  
 GTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGC  
 TTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATC  
 CAGAGCCAGATCACGCCCCATGCCATCATCTTCCTCCCCAACACCGACGGCATGGAGATG  
 CTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAAGGAT  
 GTGGTGTGCTGAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATA  
 ATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGG  
 GTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTG  
 TTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGT  
 AACCGCATCATGAACTGGTGACGGGGCCCTGGGCTGGGGCTGTCCACACTGGACCCAGC  
 TCTCCCCCTGCAGCCAGGCTTCCCGGGCCGCCCTCTTTCCCTCCCTGGGCTTTTGCTT  
 TTAAGTGGTTTGATTTCACTGGAGCCTGCTGGGAACGTGACCTCTGACCCCTGA

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CAATGTAAACCCACTCTATGTCTCTCCTGCATGTAAAAAACCCTAATCCACATGTATGA  
 AAAGGAGTTCACCTTCTGAGATCTGCTGTGGTTCTTTGTGGGGAGTCAATTTGCTGTTGGG  
 AACCCGATCTAATCTATATCTGATGGACAGAAGTGGAAAGGCTGACATTACTAACTTAT  
 AAGGCCGAAGACCATTCCGCCAGATTCAAGTCTTAGAGCCACTCAATTTGCTGATTACCAT



CTCAGGTCATAAGAACAGACTTCGGGTGTATCATCTGACCTGGTTGAGGAACAAGATTTT  
 GAATAATGATCCAGAAAGTAAAAGAAGGCAAGAAGAAATGCTGAAGACAGAGGAAGCCTG  
 CAAAGCTATTGATAAGTTAACAGGCTGTGAACACTTCAGTGTCTCCAACATGAAGAAAC  
 AACATATATTGCAATTGCTTTGAAATCATCAATTCACCTTTATGCATGGGCACCAAAGTC  
 CTTTGATGAAAGCACTGCTATTAAAGTATTTCCAACACTTGATCATAAGCCAGTGACAGT  
 TGACCTGGCTATTGGTTCTGAAAAAAGACTAAAGATTTTCTTCAGCTCAGCAGATGGATA  
 TCACCTCATCGATGCAGAATCTGAGGTTATGTCTGATGTGACCCTGCCAAAGAATCCCCCT  
 GGAAATCATTATACCACAGAATATCATCATTTTACCTGATTGCTTGGGAATTGGCATGAT  
 GCTCACCTTCAATGCTGAAGCCCTCTCTGTGGAAGCAAATGAACAACCTCTTCAAGAAGAT  
 CCTTGAAATGTGGAAAGACATAACCATCTTCTATAGCTTTTGAATGTACACAGCGAACCAC  
 AGGATGGGGCCAAAAGGCCATTGAAGTGCGCTCTTTGCAATCCAGGGTTCTGGAAAGTGA  
 GCTGAAGCGCAGGTCAATTAAGAAGCTGAGATTCTGTGCACCCGGGGTGACAAGCTGTT  
 CTTTACCTCTACCCTGCGCAATCACCACAGCCGGGTTTACTTCATGACACTTGGAAAAC  
 TGAAGAGCTCCAAAGCAATTATGATGTCTAAAAGTTTCCAGTGATTTATTACCACATTAT  
 AAACATCATGTATAGGCAGTCTGCATCTTCAGATTTTCAGAGATTAAATGAGTATTCAGTT  
 TTATTTTTAGTAAAGATTAAATCCAAAACCTTTACTTTTAATGTAGCACAGAATAGTTTTA  
 ATGAGAAATGCAGCTTTATGTATAAAATTAAGTATAGCAAGCTCTAGGTACTCCAATGGT  
 GTACAATGTCTTTTGACAAACTTTGTAACCTTTTGTTACTGTGAATTCAAACATTACTCT  
 TTGGACAGTTTGGACAGTATCTGTATTTCAGATTTTACAACATGGAGTAAAGAAACCTGTT  
 ATGAATTAGATTACAAGCAGCCTTCAAAGAATTGGCACTGGGATAAGATTTTTCAGAAA  
 AGAAAAACATCGGCCAACT

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CCGCCATGAACCCCGGCTTCGATTTGTCCCGCCGGAACCCGCAGGAGGACTTCGAGCTGA  
 TTCAGCGCATCGGCAGCGGCACCTACGGCGACGTCTACAAGGCACGGAATGTTAACACTG  
 GTGAATTAGCAGCAATTAAAGTAATAAAATTGGAACCAGGAGAAGACTTTGCAGTTGTGC  
 AGCAAGAAATTATTATGATGAAAGACTGTAAACACCCAAATATTGTTGCTTATTTTGGAA  
 GCTATCTCAGGCGAGATAAGCTTTGGATTTGCATGGAGTTTTGTGGAGGTGGTTCTTTAC  
 AGGATATTTATCACGTAAGTGGACCTCTGTCAGAACTGCAAATTGCATATGTTAGCAGAG  
 AAACACTGCAGGGATTATATTATCTTCACAGTAAAGGAAAAATGCACAGAGATATAAAGG  
 GAGCTAACATTCTATTAACGGATAATGGTCATGTGAAATTGGCTGATTTTGGAGTATCTG  
 CACAGATAACAGCTACAATTGCCAAACGGAAGTCTTTCATTGGCACACCATATTGGATGG  
 CTCCAGAAGTTGCAGCTGTTGAGAGGAAGGGGGTTACAATCAACTCTGTGATCTCTGGG  
 CAGTGGGAATCACTGCCATAGAACTTGCAGAGCTTCAGCCTCCTATGTTTGACTTACACC  
 CAATGAGAGCATTATTTCTAATGACAAAAAGCAATTTTCAGCCTCCTAAACTAAAGGATA  
 AAATGAAATGGTCAAATAGTTTTCATCACTTTGTGAAAATGGCACTTACCAAAAATCCGA  
 AAAAAAGACCTACTGCTGAAAAATTATTACAGCATCCTTTTGTAAACACAACATTTGACAC  
 GGTCTTTGGCAATCGAGCTGTTGGATAAAGTAAATAATCCAGATCATTCCACTTACCATG

**Fig. 9L**  
44/76



ATTTTCGATGATGATGATCCTGAGCCTCTTGTTGCTGTACCATAGAAATTCACCTCAACAA  
 GTAGAAACGTGAGAGAAGAAAAACACGCTCAGAGATAACCTTTGGCCAAGTGAAATTTG  
 ATCCACCCTTAAGAAAGGAGACAGAACCACATCATGAACTTCCCGACAGTGATGGTTTTT  
 TGGACAGTTT CAGAAGAAATATACTACACTGCAAGATCTAATCTGGATCTGCAACTGGAAT  
 ATGGACAAGGACACCAAGGTGGTTACTTTTTAGGTGCAACAAGAGTCTTCTCAAGTCTG  
 TTGAAGAAGAATTGCATCAGCGAGGACACGTGCGACATTTAGAAGATGATGAAGGAGATG  
 ATGATGAATCTAAACACTCAACTCTGAAAGCAAAAATTCCACCTCCTTTGCCACCAAGC  
 CTAAGTCTATCTTCATACCACAGGAAATGCATTCTACTGAGGATGAAAATCAAGGAACAA  
 TCAAGAGATGTCCCATGTCAGGGAGCCCAGCAAAGCCATCCCAAGTTCCACCTAGACCAC  
 CACCTCCCAGATTACCCCCACACAAACCTGTTGCCTTAGGAAATGGAATGAGCTCCTTCC  
 AGTTAAATGGTGAACGAGATGGCTCATTATGTCAACAACAGAATGAACATAGAGGCACAA  
 ACCTTTCAAGAAAAGAAAAGAAAGATGTACCAAAGCCTATTAGTAATGGTCTTCTCCAA  
 CACCTAAAGTGCATATGGGTGCATGTTTTTCAAAGTTTTTAATGGGTGTCCCTTGAAAA  
 TTCACTGTGCATCATCATGGATAAACCCAGATACAAGAGATCAGTACTTGATATTTGGTG  
 CCGAAGAAGGGATTTATACCCTCAATCTTAATGAACTTCATGAAACATCAATGGAACAGC  
 TATTCCTCGAAGGTGTACATGGTTGTATGTAATGAACAATTGCTTGCTATCAATATCTG  
 GTAAAGCTTCTCAGCTTTATTCCCATAATTTACCAGGGCTTTTTTGATTATGCAAGACAAA  
 TGCAAAAGTTACCTGTTGCTATTCAGCACACAAACTCCCTGACAGAATACTGCCAAGGA  
 AATTTTCTGTATCAGCAAAAATCCCTGAAACCAAATGGTGCCAGAAGTGTTGTGTTGTAA  
 GAAATCCTTACACGGGCCATAAATACCTATGTGGAGCACTTCAGACTAGCATTGTTCTAT  
 TAGAATGGGTTGAACCAATGCAGAAATTTATGTTAATTAAGCACATAGATTTTCTTATAC  
 CATGTCCACTTAGAATGTTTGAAATGCTGGTAGTTCTGAAACAGGAGTACCCTTTAGTTT  
 GTGTTGGTGTCAGTAGAGGTAGAGACTTCAACCAAGTGGTTGCTTTGAGACGGTCAATC  
 CAAATTCTACCTCTTCATGGTTTACAGAATCAGATACCCACAGACAAATGTTACTCATG  
 TAACCCAACTGGAGAGAGATAACCATCCTTGATGCTTGGACTGTTGTATAAAAATAGTAA  
 ATCTCCAAGGAAGATTAAAATCTAGCAGGAAATTGTCATCAGAACTCACCTTTGATTTC  
 AGATTGAATCAATAGTGTGCCTACAAGACAGTGTGCTAGCTTTCTGGAAACATGGAATGC  
 AAGGTAGAAGTTTTAGATCTAATGAGGTAACACAAGAAATTTAGATAGCACAGAATTT  
 TCAGGCTGCTTGGATCTGACAGGGTCGTGGTTTTGGAAAGTAGGCCAACTGATAACCCCA  
 CAGCAAATAGCAATTTGTACATCCTGGCGGGTCATGAAAACAGTTACTGAGAATTGTTGT  
 GCTTTGACAGTTAACTCTAGAAAGAAAGAACTACCACTGCAACATTAATGGATGCTTG  
 AAGCTGTACAAAAGCTGCAGTAACCTGTCTTCAGTTACTTTGTAATTTATTGTGGCATGA  
 GATAAGATGGGGAAAATTTTGTTTTAAGTGGTATGGATATATTTAGCATATTGAACCACA  
 CAAGTGCTTAATTCATTGTTATGTAATCTTTGTACATATAGGCAGTATTTTTCTGTGAA  
 ACTTCATATTGCTGAAGACATACACTAAGAATTTATGTAGATAATGTACTTTTATGAGAT  
 GTACAAGTAAGTGTCTTATCTGTACAGATGTAAATGTTGATGAAAATGCAATTGGGGTTA  
 ATATTTTAAGAATCTTTAGTATATTCTTGGGTGTGGCTATATTACAAAATGGGATGCTG  
 GCAATGAAACAATACATTTAACAATTTGATTTTTATTATATGTAATTTAGTAATATGA

ATATAAATCTTGTAACCTTTTAAAATTGTAATGGAGGCTGTAATCATTTTATAATCTTTTT  
AATTTTAATGCAAGTACACTGGTGTATTTATATTTGCACAAAGTATTGATATGTGATGTATT  
AAGTCACAAAAGTAAGCTGTGACATTGTCTATAAGCATTGGCTCCACAAATGTATTTGG  
ATTGTTTTCTATGTGAAGCAAACCAATTATAATTAACCACATGTTGTAGTAACTGGTCTT  
TTTATATTTAAGCAGAATCCTGTAAGATTGCTTGTCTTTGCTTAAAAACAATACCTTTGA  
ACATTTTTGAATCACAGAATAGCGGTACCATGATAGAATACTGCAATTGTGGTCAGAATT  
ACAGTATGCACAAAGAATTAATTAGCATTATTAAGAGAGTCTCACTAAACATTTTCATATG  
ATCACACTGAAGAACTGTAACATTCCATAGAGTGAAGTGGTTCAAATTTCTCTTGGAATT  
TTTACTTTTGTGGCCTTATTTTATGATCCTTTTCATATTTCTTTTGACTTAGAGTATTA  
ATACATGGCCAAAATAATTTAGTTACTACCTCATACAAACAATATAATGGTTACTACACA  
TCACAGGAAGCTTAGTTTTGGTTTTAAGTCAFTTTTGATTGCTTTTTTCCAATGGAATATGT  
ATATACCAGGTTTTAGCAAAATGCACACTTTTGGCTCTTTTTGGTATATGTTCTTTATAT  
TTTAATGTGAGTATATACACTAAGAACAACCTAAATTGTGATTTATGATCTTCATTTATT  
TTAATGATAATGGTTTTAAAATATGTTCTGATTGTACATATTGTAAATAAACATGTTT  
TTT

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GGGAGGGTCCTTGTGGCGCCGGGCGGGGTCCTGCGTGGAGAGTGGGACGCAACGCCG  
AGACCGCGAGCAGAGGCTGCGCACAGCCGGATCCGGCACTCAGCGACCGGACCCAAGGAT  
CCGCCGGGGAACAAGCCACAGGAGAGCGACTCAGGAACAAGTGTGGGAGAGGAAGCGGCG  
GCGGCGGCGCCGGGCCCCGGGGGTGGTGACAGCAGGTCTGAGGTTGCATCATAAATACAAA  
GGACTGAAGTTATAAAAAGAGAAAAGAGAAGTTTGCTGCTAAAATGAATCTGAGCAATATG  
GAATATTTTGTGCCACACACAAAAAGGTACTGAAGATTTACCCCCCAAAAAAATTGTCA  
ATGAGAAATAAAGCTAACTGATATCAAAAAGCAGAGCCTGCTCTACTGGCCATCATGCGT  
AAAGGGGTGCTGAAGGACCCAGAGATTGACGATCTATTCTACAAAGATGATCCTGAGGAA  
CTTTTTATTGGTTTGCATGAAATTGGACATGGAAGTTTTGGAGCAGTTTATTTTGCTACA  
AATGCTCACACCAATGAGGTGGTGGCAATTAAGAAGATGTCCTATAGTGGGAAGCAGACC  
CATGAGAAATGGCAAGATATTCTTAAGGAAGTTAAATTTTTACGACAATTGAAGCATCCT  
AATACTATTGAGTACAAAGGCTGTTACTTGAAAGAACACACTGCTTGGTTGGTGATGGAA  
TATTGCTTAGGCTCAGCCTCTGATTTATTAGAAGTTCATAAAAAACCACTTCAGGAAGTG  
GAGATCGCTGCCATTACTCATGGAGCCTTGCATGGACTAGCCTACCTACATTCTCATGCA  
TTGATTCATAGGGATATTAAAGCAGGAAATATTCTTCTAACAGAGCCAGGTCAGGTAAAA  
CTAGCTGATTTTGGATCTGCTTCAATGGCTTCTCCTGCCAACTCCTTCGTGGGCACACCT  
TACTGGATGGCTCCAGAGGTGATCTTAGCTATGGATGAAGGACAGTATGATGGGAAAGTT  
GATATTTGGTCACTTGGCATCACTTGTATTGAATTGGCGGAACGGAAGCCGCCCTTTTC  
AACATGAATGCAATGAGTGCCTTATATCACATTGCCCAGAATGACTCCCCAACGTTACAG  
TCTAATGAATGGACAGACTCCTTTAGGAGATTTGTTGATTACTGCTTGCAGAAAATACCT  
CAGGAAAGGCCAACATCAGCAGAACTATTAAGGCATGACTTTGTTCGACGAGACCGGCCA

CTACGTGTCCTCATTGACCTCATACAGAGGACAAAAGATGCAGTTCGTGAGCTAGATAAC  
 CTACAGTACCGAAAAATGAAAAAATACTTTTCCAAGAGACACGGAATGGACCCTTGAAT  
 GAGTCACAGGAGGATGAGGAAGACAGTGAACATGGAACCAGCCTGAACAGGGAAATGGAC  
 AGCCTGGGCAGCAACCATTCCATTCCAAGCATGTCCGTGAGCACAGGCAGCCAGAGCAGC  
 AGTGTGAACAGCATGCAGGAAGTCATGGACGAGAGCAGTTCCGAACCTTGTCATGATGCAC  
 GATGACGAAAGCACAAATCAATTCCAGCTCCTCCGTGCGTGCATAAGAAAGATCATGTATTC  
 ACAAGGGATGAGGCGGGCCACGGCGATCCCAGGCCTGAGCCGCGGCCTACCCAGTCAGTT  
 CAGAGCCAGGCCCTCCACTACCGGAACAGAGAGCGCTTTGCCACGATCAAATCAGCATCT  
 TTGGTTACACGACAGATCCATGAGCATGAGCAGGAGAACGAGTTGCGGGAACAGATGTCA  
 GGTTATAAGCGGATGCGGCGCCAGCACCAGAAGCAGCTGATCGCCCTGGAGAACAAAGCTG  
 AAGGCTGAGATGGACGAGCACCGCCTCAAGCTACAGAAGGAGGTGGAGACGCATGCCAAC  
 AACTCGTCCATCGAGCTGGAGAAGCTGGCCAAGAAGCAAGTGGCTATCATAGAAAAGGAG  
 GCAAAGGTAGCTGCAGCAGATGAGAAGAAGTTCCAGCAACAGATCTTGGCCCAGCAGAAG  
 AAAGATTTGACAACTTTCTTAGAAAGTCAGAAGAAGCAGTATAAGATTTGTAAGGAAAAA  
 ATAAAAGAGGAAATGAATGAGGACCATAGCACACCCAAGAAAGAGAAGCAAGAGCGGATC  
 TCCAAACATAAAGAGAACTTGCAGCACACACAGGCTGAAGAGGAAAGCCCACCTTCTCACT  
 CAACAGAGACTGTACTACGACAAAAATTGTCGTTTCTTCAAGCGGAAAATAATGATCAAG  
 CGGCACGAGGTGGAGCAGCAGAACATTCGGGAGGAACTAAATAAAAAGAGGACCCAGAAG  
 GAGATGGAGCATGCCATGCTAATCCGGCACGACGAGTCCACCCGAGAGCTAGAGTACAGG  
 CAGCTGCACACGTTACAGAAGCTACGCATGGATCTGATCCGTTTACAGCACCCAGACGGAA  
 CTGGAAAACCAGCTGGAGTACAATAAGAGGGCGAGAAAGAGAACTGCACAGAAAGCATGTC  
 ATGGGACTTCGGCAACAGCCAAAAAACTTAAAGGCCATGGAAATGCAAATTAAAAAACAG  
 TTTCAGGACACTTGCAAAGTACAGACCAAACAGTATAAAGCACTCAAGAATCACCAGTTG  
 GAAGTTACTCCAAAGAATGAGCACAAAACAATCTTAAAGACACTGAAAGATGAGCAGACA  
 AGAAAACCTTGCCATTTTGGCAGAGCAGTATGAACAGAGTATAAATGAAATGATGGCCTCT  
 CAAGCGTTACGGCTAGATGAGGCTCAAGAAGCAGAATGCCAGGCCTTGAGGCTACAGCTC  
 CAGCAGGAAATGGAGCTGCTCAACGCCTACCAGAGCAAAATCAAGATGCAAACAGAGGCA  
 CAACATGAACGTGAGCTCAGAAAGCTAGAGCAGAGAGTGTCTCTGCGCAGAGCACACCTT  
 GAGCAGAAGATTGAAGAGGAGCTGGCTGCCCTTCAGAAGGAACGCAGCGAGAGAATAAAG  
 AACCTATTGGAAAGGCAAGAGCGAGAGATTGAAACTTTTGACATGGAGAGCCTCAGAATG  
 GGATTTGGGAATTTGGTTACATTAGATTTTCTAAGGAGGACTACAGATGAGATTAAATT  
 TTTTGCCATTTACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
 AACCACATTCCCCATTTTAACGGGCGTTGCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCT  
 ACATCGTGTGCGACTAGTGCTGTTTATTCTTACTCCATCAGGGGGCCCCCTTCTCCCCC  
 CGTGTCAACTTTTCAAGTGCTGGCCAAAACCTGGCCGTCTCTTCTATTACAGTACACGTCA  
 CAGTATTGATGTGATTCAAAATGTTTCAGTGAAAACCTTTGGAGACAGTTTAAACAAAACC  
 AATAAACCAACAACAAAAAAAGTGGATGTATATTGCTTTAAGCAATCACTCATTACCACC  
 AATCTGTGAAAGTAAAGCAAAAAATAATAATAATAATAATGCCAAGGGGGAGAGAGACACAA

**Fig. 9 O**  
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TATCCGCAGCCTTACACCTTAACTAGCTGCTGCATTATTTTATTTTATTTTATTTTATTTT  
GTATTTATTCATCAGGAATAAAAAAACAAGTTTTATTAAAGATTGAAAATTTGATACA  
TTTACAGAACTAATTGTGATGTACATATCAGTGGTGACATATTATTACTTTTTTGGGG  
ACGGGGGGTGGGTGGGTGAAGAGATCTTGTGATTTTTTAAGAACCTGCTGGCAAGAGTT  
AACTTGTCTTCAGCATATTCTGATTGTATCATAATCATTTTCTGCTGTTGCAGAGGATGT  
GAATACACTTAAGGAGCTCACAGAATCCCAGTAGCACAAATTGGGCTTTGGCAAATCGTG  
TATTTTGTGTATAGAAGGAATTTAAGGAGAGGTATTACTTATTTTCATATTGTATTTTAA  
CTGTTTCTCTGATCAAATTTTTTTTACTTCCTCCTCCTGTTCTCCCCACCTCCCTCCTT  
TCCAGTTCAGTATTTGGAGTTCAACACTGTCTCTCAATCAGATCATCTTGATCTTTTTCT  
TTATCTCCCTTCCCCTTCTAAGTCCCATTCTTGGTCATAAATATTGCATTATTCACAC  
TTTCAAACCTGTGTATTTTCTTACAATAAAAAATGATGAAAAAAAAAAAAAAAAAAAA

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TATTGAATTGGCGGAACGGAAGCCTCCTTTATTTAATATGAATGCAATGAGTGCCTTATA  
TCACATAGCCCAAATGAATCCCCTACACTACAGTCTAATGAATGGTCTGATTATTTTCG  
CAACTTTGTAGATTCTTGCCTCCAGAAAATCCCTCAAGATCGACCTACATCAGAGGAACT  
TTTAAAGCACATATTTGTTCTTCGGGAGCGCCCTGAAACCGTGTTAATAGATCTCATTCA  
GAGGACAAAGGATGCAGTAAGAGAGCTGGACAATCTGCAGTATCGAAAGATGAAGAACT  
CCTTTTCCAGGAGGCACATAATGGACCAGCAGTAGAAGCACAGGAAGAAGAAGAGGAACA  
AGATCATGGTGTGGCCGGACAGGAACAGTTAATAGTGTTGGAAGTAATCAATCCATTCC  
CAGCATGTCCATCAGTGCCAGCAGCCAAAGCAGTAGTGTTAACAGTCTTCCAGATGTCTC  
AGATGACAAGAGTGAGCTAGACATGATGGAGGGAGACCACACAGTGATGTCTAACAGTTC  
TGTTATCCATTTAAAACAGAGGAAGAAAATTACAGAGAAGAGGGAGATCCTAGAACAAG  
AGCATCAGATCCACAATCTCCACCCCAAGTATCTCGTCACAAATCACACTATCGTAATCG  
AGAACACTTTGCTACTATACGGACAGCATCACTGGTTACGAGGCAAATGCAAGAACATGA  
GCAGGACTCTGAGCTTAGAGAACAATGTCTGGCTATAAGCGAATGAGGCGACAACATCA  
AAAGCAACTGATGACTCTGGAAAACAAGCTAAAGGCTGAGATGGATGAACATCGCCTCAG  
ATTAGACAAAGATCTTGAAACTCAGCGTAACAATTTTGCTGCAGAAATGGAGAACTTAT  
CAAGAAACACCAGGCTGCCATGGAGAAAGAGGCTAAAGTGATGTCCAATGAAGAGAAAAA  
ATTTAGCAACATATTCAGGCCCAACAGAAGAAAGAACTGAATAGTTTTCTCGAGTCCCA  
GAAAAGAGAGTATAAACTTCGAAAAGAGCAGCTTAAAGAGGAGCTAAATGAAAACAGAG  
TACCCCAAAAAAGAAAAACAGGAGTGGCTTTCAAAGCAGAAGGAGAATATACAGCATT  
CCAAGCAGAAGAAGAAGCTAACCTTCTTCGACGTCAAAGACAATACCTAGAGCTGGAATG  
CCGTCGCTTCAAGAGAAGAATGTTACTTGGGCGTCATACTTAGAGCAGGACCTTGTCAG  
GGAGGAGTTAAACAAAAGACAGACTCAGAAGGACTTAGAGCATGCCATGCTACTCCGACA  
GCATGAATCTATGCAAGAACTGGAGTTCGCCACCTCAACACAATTCAGAAGATGCGCTG  
TGAGTTGATCAGATTACAGCATCAAACCTGAGCTCACTAACCAGCTGGAATATAATAAGCG  
AAGAGAACGAGAATAAGACGAAAGCATGTCATGGAAGTTCGACAACAGCCTAAGAGTTT

Title: NUCLEIC ACIDS ENCODING  
PAK5 POLYPEPTIDES AND  
METHODS OF USE THEREOF  
Inventor(s): Gregory PLOWMAN et al.  
DOCKET NO.: 034536-1034

**Fig. 9P**  
48/76

GAAGTCTAAAGAACTCCAAATAAAAAAGCAGTTTCAGGATACCTGCAAAATCCAAACCAG  
 ACAGTACAAAGCATTAAGAAATCACCTGCTGGAGACTACACCAAAGAGTGAGCACAAAGC  
 TGTCTGAAACGGCTCAAGGAGGAACAGACCCGGAAATTAGCTATCTTGGCTGAGCAGTA  
 TGATCACAGCATTAAATGAAATGCTCTCCACACAAGCCCTGCGTTTGGATGAAGCACAGGA  
 AGCAGAGTGCCAGGTTTTGAAGATGCAGCTGCAGCAGGAACTGGAGCTGTTGAATGCGTA  
 TCAGAGCAAAATCAAGATGCAAGCTGAGGCACAACATGATCGAGAGCTTCGCGAGCTTGA  
 ACAGAGGGTCTCCCTCCGGAGGGGCACTCTTAGAACAAAAGATTGAAGAAGAGATGTTGGC  
 TTTGCAGAATGAGCGCACAGAACGAATACGAAGCCTGTTGGAACGTCAAGCCAGAGAGAT  
 TGAAGCTTTTGA CTCTGAAAGCATGAGACTAGGTTTTAGTAATATGGTCTTTCTAATCT  
 CTCCCCTGAGGCATTTCAGCCACAGCTACCCGGGAGCTTCTGGTTGGTCACACAACCCTAC  
 TGGGGGTCCAGGACCTCACTGGGGTCATCCCATGGGTGGCCACCAAGCTTGGGGCCA  
 TCCAATGCAAGGTGGACCCCAAGCCATGGGGTCACCCTTCAGGGCCAATGCAAGGGGTACC  
 TCGAGGTAGCAGTATGGGAGTCCGCAATAGCCCCCAGGCTCTGAGGGCGGACAGCTTCTGG  
 GGGACGGACGGAGCAGGGCATGAGCAGAAGCACGAGTGTCACTTCACAAATATCCAATGG  
 GTCACACATGTCTTATACATAACTTAATAATTGAGAGTGGCAATTCGCTGGAGCTGTCT  
 GCCAAAAGAACTGCCTACAGACATCATCACAGCAGCCTCCTCACTTGGGTACTACAGTG  
 TGGAAAGCTGAGTGCATATGGTATATTTTATTCATTTTTGTAAAGCGTTCTGTTTTGTGTT  
 TACTAATTGGGATGTCATAGTACTTGGCTGCCGGGTTTGTGTTGTTTGGGGAAATTTTG  
 AAAAGTGGAGTTGATATTAATAATAATGTGTATGTGTGTACATATATATACACACACAT  
 ACACATATATTATGCATGTGGTGAAGAATTGGCTAGATAGGGGATTTTTCTGAACACT  
 GCAAAAATAGAACGTAGCAAAATGGCTTCAGTTATCACTTTTGGGTGTCTGTATCCTAAG  
 AAGTTTCTGAAAAGATCTAAAGCCTTTTTATCCCATATCCCAAATTCTTATGAGCCACTC  
 ACAGCAGGCAGCATATGTTGAAATAAGTTATTACTGGTACACACCTGCATTGCCTCACCA  
 GTGTATTTATTTGTTATTAAATTGATCTGACTTCTCAGCCTCATTGGACTAAAAAAGA  
 AAGCAGAAATCCATGAACACATTGCTTCTCGGCCTTTTGGCTAAGATCAAGTGTAGAAAT  
 CCATGAACACTAAAGGACTTCATTGATTTTTTCAGAGAGTAGAAAACAACCTTAGTTTTTC  
 TTTTTCTGAAATGCGTCATAGGCTTGTGAGTGATTTTTGTCCATTCAATTGTGCCTTCT  
 TTGTATTATGATAAGATGGGGGTACTTAAGGAGATCACAAGTTGTGTGAGGATTGCATTA  
 ACAAACCTATGAGCCTTCAATGGGGAAGACCAGAAGGGTGAGAGGGGGCCCTGAAAGTTCA  
 TATGGTGGGTATGTCCCGCAGCAGAGTGAGGAGATGAAGCTTACGTGTCCTGACGTTTTG  
 TTGCTTATACTGTGATATCTCATCCTAGCTAAGCTCTATAATGCCCAAGACCCCAAACAG  
 TACTTTTACTTTGTTTGTACAAAAACAAAGACATATAGCCAATACAAATCAAATGCCGGA  
 GGTGTTTGATGCCATATTTGCAAATTGCCATCTATTGAAATTCTCGTCACACTACATAGA  
 CATAATTGTTATCTCCTTTTGGCTTATGTGATTTTCTGTTTACAAGTAGAATAGCCAATT  
 ATTTAAATGTTTAGTTGCCACAGTGAACCAGGAGTCACTGAGCCAATGACTTTACCAGCT  
 GCTGACTAATCTTCATCACCCTGTAGATTTTGTGCTGCATGTGCAGGTCCTCTATTTTTAA  
 TTGCTGTTTTCGTTGCTGCAGTACTTTACAACTTCTAGTTGTTGAGACTTAGTGACCA  
 TTTGGCATCAAGTTAACATCACACAATAGGAAACACCACTTCCACAAGTCTCAAGCCTCA

Title: NUCLEIC ACIDS ENCODING  
 PAK5 POLYPEPTIDES AND  
 METHODS OF USE THEREOF  
 Inventor(s): Gregory PLOWMAN et al.  
 DOCKET NO.: 034536-1034

**Fig. 9Q**  
 49/76

GTGCTAAAGTACTACTGAAAAGGAACTAGGAAGTTTGGCCAATT

SEQ ID NO: 21 SULU3 MURINE

GCAGGATGCCATCAACTAACAGAGCAGGCAGTCTAAAGGACCCTGAAATTGCAGAGCTCT  
TCTTCAAAGAAGATCCGGAAAAGCTCTTCACAGATCTCAGAGAAATCGGCCATGGGAGCT  
TTGGAGCAGTATATTTTGCACGAGATGTGCGTACTAATGAAGTGGTGGCCATCAAGAAAA  
TGTCTTATAGTGGAAGCAGTCTACTGAGAAATGGCAGGATATTATTAAGGAAGTCAAGT  
TTCTACAAAGAATAAAACATCCCAACAGTATAGAATACAAAGGCTGCTATTTACGTGAAC  
ACACAGCATGGCTTGTAATGGAATATTGTTTAGGATCTGCTTCAGATTTATTAGAAGTTC  
ATAAAAAGCCATTACAAGAAGTGGAAATAGCAGCAATTACACATGGTGCTCTCCAGGGAC  
TAGCTTATTTACATTCTCATAACCATGATCCATAGAGATATCAAAGCAGGAAATATCCTTC  
TGACAGAACCAGGCCAAGTGAAACTTGCTGACTTTGGATCTGCTTCCATGGCTTCCCCTG  
CCAATTCTTTTGTGGGAACACCATATTGGATGGCCCCAGAAGTAATTTTAGCCATGGATG  
AAGGACAGTATGATGGCAAAGTTGATGTATGGTCTCTTGGAATAACGTGTATTGAATTAG  
CCGAGAGGAAGCCTCCTTTATTTAATATGAATGCAATGAGTGCCTTATATCACATAGCCC  
AAAATGAATCCCCTACACTACAATCTAATATGAATGATTCTTGCCCTCCAGAAAATCCCTC  
AAGATCGCCCTACATCAGAGGAACTTTTAAAGCACATGTTTGTTCCTTCGAGAGCGCCCTG  
AAACAGTGTTAATAGATCTTATTCAAAGGACAAAGGATGCAGTAAGAGAGCTGGACAATC  
TGCAGTATCGAAAGATGAAGAACTCCTTTTCCAGGAGGCACATAATGGGCCAGCGGTAG  
AAGCACAGGAAGAAGAGGAGGAGCAAGATCATGGTGTTGGCCGAACAGGAACAGTGAATA  
GTGTTGGAAGCAATCAGTCTATCCCTAGTATGTCTATCAGTGCCAGCAGTCAAAGCAGCA  
GTGTTAATAGTCTTCCAGATGCATCAGATGACAAGAGTGAGCTAGACATGATGGAGGGAG  
ACCATACAGTGATGTCTAACAGTTCTGTCTATCCACTTAAACCTGAGGAGGAAAATTACC  
AGGAAGAAGGAGATCCTAGAACAAAGAGCATCAGACCCACAGTCTCCCCCTCAGGTGTCTC  
GTCACAAGTCACATTATCGTAATAGAGAACACTTTGCAACCATACGAACAGCATCACTGG  
TTACAAGACAGATGCAAGAACATGAGCAGGACTCTGAACTTAGAGAACAGATGTCTGGTT  
ATAAGCGGATGAGGCGACAGCATCAAAAGCAGCTGATGACGCTGGAAAATAAACTGAAGG  
CAGAGATGGACGAACATCGGCTCAGATTAGACAAAGATCTTGAAACTCAGCGTAACAATT  
TCGCTGCAGAAATGGAGAACTTATTAAGAAACACCAAGCTGCTATGGAAAAAGAGGCTA  
AAGTGATGGCCAATGAGGAGAAAAAATTCCAGCAACACATTCAGGCTCAACAGAAAAAG  
AACTGAATAGCTTTTTTGGAGTCTCAAAAAAGAGAATATAAACTTCGCAAAGAGCAGCTTA  
AGGAGGAGCTGAATGAAAACCAGAGCACACCTAAAAAAGAAAAGCAGGAATGGCTTTCAA  
AGCAGAAGGAGAATATACAGCATTTTTCAGGCAGAAGAAGAAGCTAATCTTCTTCGACGTC  
AAAGGCAGTATCTAGAGCTAGAATGTCGTCGCTTCAAAAGAAGAATGTTACTTGGGCGAC  
ATAACTTGGAACAGGACCTTGTCAGGGAGGAGTTAAACAAAAGGCAGACTCAAAGGACT  
TGGAACATGCAATGCTATTGCGACAGCATGAATCAATGCAAGAACTGGAGTTTCGCCATC  
TCAACACTATTGAGAAGATGCGCTGTGAGTTGATCAGACTGCAGCATCAAACCTGAGCTCA  
CTAACAGCTAGAGTACAATAAGAGAAGGGAACGGGAACTGAGGCGAAAACATGTCATGG

AAGTTCGACAACAACCTAAGAGTCTGAAGTCTAAAGAACTCCAAATAAAAAAGCAGTTTC  
AGGATACCTGCAAAATTCAAAACAGACAGTACAAAGCATTAAAGGAATCACCTACTGGAGA  
CTACACCAAAGAATGAGCACAAAGCAATC

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CGAAGCCACAGCCCGAGCCCGAGCCCGAGCCCGAGCCGGCGCCACCGCGCCCCCGGCCAT  
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CGAATATGAGCACGTCCGCGCGACCTGGACCCCAACGAGGTGTGGGAGATCGTGGGCGA  
GCTGGGCGACGGCGCCTTCGGCAAGGTTTACAAGGCCAAGAATAAGGAGACGGGTGCTTT  
GGCTGCGGCCAAAGTCATTGAAACCAAGAGTGAGGAGGAGCTGGAGGACTACATCGTGGA  
GATTGAGATCCTGGCCACCTGCGACCACCCCTACATTGTGAAGCTCCTGGGAGCCTACTA  
TCACGACGGGAAGCTGTGGATCATGATTGAGTTCTGTCCAGGGGGAGCCGTGGACGCCAT  
CATGCTGGAGCTGGACAGAGGCCTCACGGAGCCCCAGATACAGGTGGTTTGGCGCCAGAT  
GCTAGAAGCCCTCAACTTCCTGCACAGCAAGAGGATCATCCACCGAGATCTGAAAGCTGG  
CAACGTGCTGATGACCCTCGAGGGAGACATCAGGCTGGCTGACTTTGGTGTGTCTGCCAA  
GAATCTGAAGACTCTACAGAAACGAGATTCTTTCATCGGCACGCCTTACTGGATGGCCCC  
CGAGGTGGTCATGTGTGAGACCATGAAAGACACGCCCTACGACTACAAAGCCGACATCTG  
GTCCCTGGGCATCACGCTGATTGAGATGGCCCAGATCGAGCCGCCACACCACGAGCTCAA  
CCCCATGCGGGTCCTGCTAAAGATCGCCAAGTCGGACCCTCCCACGCTGCTCACGCCCTC  
CAAGTGGTCTGTAGAGTTCCGTGACTTCCTGAAGATAGCCCTGGATAAGAACCCAGAAAC  
CCGACCCAGTGCCGCGCAGCTGCTGGAGCATCCCTTCGTGAGCAGCATCACCAGTAACAA  
GGCTCTGCGGGAGCTGGTGGCTGAGGCCAAGGCCGAGGTGATGGAAGAGATCGAAGACGG  
CCGGGATGAGGGGGAAGAGGAGGACGCCGTGGATGCCGCCTCCACCCTGGAGAACCATAC  
TCAGAACTCCTCTGAGGTGAGTCCGCCAAGCCTCAATGCTGACAAGCCTCTCGAGGAGTC  
ACCTTCCACCCCGCTGGCACCCAGCCAGTCTCAGGACAGTGTGAATGAGCCCTGCAGCCA  
GCCCTCTGGGGACAGATCCCTCCAAACCACAGTCCCCCAGTCGTGGCCCCCTGGAAATGA  
GAACGGCCTGGCAGTGCCCTGTGCCCCTGCGGAAGTCCCGACCCGTGTCAATGGATGCCAG  
AATTCAGGTAGCCCAGGAGAAGCAAGTTGCTGAGCAGGGTGGGGACCTCAGCCCAGCAGC  
CAACAGATCTCAAAAGGCCAGCCAGAGCCGGCCCAACAGCAGCGCCCTGGAGACCTTGGG  
TGGGGAGAAGCTGGCCAATGGCAGCCTGGAGCCACCTGCCCAGGCAGCTCCAGGGCCTTC  
CAAGAGGGACTCGGACTGCAGCAGCCTCTGCACCTCTGAGAGCATGGACTATGGTACCAA  
TCTCTCCACTGACCTGTCGCTGAACAAAGAGATGGGCTCTCTGTCCATCAAGGACCCGAA  
ACTGTACAAAAAACCTCAAGCGGACACGCAAATTTGTGGTGGATGGTGTGGAGGTGAG  
CATCACCACTCCAAGATCATCAGCGAAGATGAGAAGAAGGATGAGGAGATGAGATTTCT  
CAGGCGCCAGGAACTCCGAGAGCTTCGGCTGCTCCAGAAAGAAGAGCATCGGAACCAGAC  
CCAGCTGAGTAACAAGCATGAGCTGCAGCTGGAGCAAATGCATAAACGTTTTGAACAGGA  
AATCAACGCCAAGAAGAAGTTCTTTGACACGGAATTAGAGAACCTGGAGCGTCAGCAAAA  
GCAGCAAGTGAGAGAAGATGGAGCAAGACCATGCCGTGCGCCCGCGGGAGGAGGCCAGGCG

Title: NUCLEIC ACIDS ENCODING  
PAK5 POLYPEPTIDES AND  
METHODS OF USE THEREOF  
Inventor(s): Gregory PLOWMAN et al.  
DOCKET NO.: 034536-1034

**Fig. 9S**  
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GATCCGCCTGGAGCAGGATCGGGACTACACCAGGTTCCAAGAGCAGCTCAAACCTGATGAA  
GAAAGAGGTGAAGAACGAGGTGGAGAAGCTCCCCGACAGCAGCGGAAGGAAAGCATGAA  
GCAGAAGATGGAGGAGCACACGCAGAAAAAGCAGCTTCTTGACCGGGACTTTGTAGCCAA  
GCAGAAGGAGGACCTGGAGCTGGCCATGAAGAGGCTCACCACCGACAACAGGCGGGAGAT  
CTGTGACAAGGAGCGCGAGTGCCTCATGAAGAAGCAGGAGCTCCTTCGAGACCGGGGAAGC  
AGCCCTGTGGGAGATGGAAGAGCACCAGCTGCAGGAGAGGCACCAGCTGGTGAAGCAGCA  
GCTCAAAGACCACTACTTCCTCCAGCGGCACGAGCTGCTGCGCAAGCATGAGAAGGAGCG  
GGAGCAGATGCAGCGCTACAACCAGCGCATGATAGAGCAGCTGAAGGTGCGGCAGCAACA  
GGAAAAGGCGCGGCTGCCCAAGATCCAGAGGAGTGAGGGCAAGACGCGCATGGCCATGTA  
CAAGAAGAGCCTCCACATCAACGGCGGGGGCAGCGCAGCTGAGCAGCGTGAGAAGATCAA  
GCAGTTCTCCCAGCAGGAGGAGAAGAGGCAGAAGTCGGAGCGGCTGCAGCAACAGCAGAA  
ACACGAGAACCAGATGCGGGACATGCTGGCGCAGTGCAGAGCAACATGAGCGAGCTGCA  
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CGTTCCTGGGCTTCCCGCTCCGCAGGCCTGCGGAGGACTGGCCCAGCAAGGTCCCAGGTC  
TTCCCTCTCCTTAGCGCCTAAGAGAGAGGGCCAGTGCGGGTGAGGAGTCGCGAGGAAGAG  
GCGGAAGGCGCCGGAAGGCACCATGTTCCGCAAGAAAAAGAAGAAACGCCCTGAGATCTC  
AGCGCCACAGAACTTCCAGCACCGTGTCCACACCTCCTTCGACCCCAAAGAAGGCAAGTT  
TGTGGGCCTCCCCCACAATGGCAGAACATCCTGGACACACTGCGGGCGCCCCAAGCCCGT  
GGTGGACCCTTCGCGAATCACACGGGTGCAGCTCCAGCCCATGAAGACAGTGGTGCGGGG  
CAGCGCGATGCCTGTGGATGGCTACATCTCGGGGCTGCTCAACGACATCCAGAAGTTGTC  
AGTCATCAGCTCCAACACCCTGCGTGGCCGCAGCCCCACCAGCCGGCGGGGCACAGTC  
CCTGGGGCTGCTGGGGGATGAGCACTGGGCCACCGACCCAGACATGTACCTCCAGAGCCC  
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GCAGCTGGGTGCCTGCCTGCAGAGCTCCCCACCAGGAGCCTCGCCCCCACGGGCACCAA  
TAGGCATGGAATGAAGGCTGCCAAGCATGGCTCTGAGGAGGGCCCGGCCACAGTCCTGCCT  
GGTGGGCTCAGCCACAGGCAGGCCAGGTGGGGAAGGCAGCCCTAGCCCTAAGACCCGGGA  
GAGCAGCCTGAAGCGCAGGCTATTCCGAAGCATGTTCTGTCCACTGCTGCCACAGCCCC  
TCCAAGCAGCAGCAAGCCAGGCCCTCCACCACAGAGCAAGCCCAACTCCTCTTTCCGACC  
GCCGCAGAAAGACAACCCCCCAAGCCTGGTGGCCAAGGCCCAGTCCTTGCCCTCGGACCA  
GCCGGTGGGGACCTTCAGCCCTCTGACCACTTCGGATAACAGCAGCCCCCAGAAGTCCCT  
CCGCACAGCCCCGGCCACAGGCCAGCTTCCAGGCCGGTCTTCCCCAGCGGGATCCCCCG  
CACCTGGCACGCCCAGATCAGCACCAAGCAACCTGTACCTGCCCCAGGACCCCCACGGTTGC  
CAAGGGTGCCCTGGCTGGTGGAGACACAGGTGTTGTGACACATGAGCAGTTCAAGGCTGC



GCTCAGGATGGTGGTGGACCAAGGGTGACCCCCGGCTGCTGCTGGACAGCTACGTGAAGAT  
 TGGCGAGGGGCTCCACCGGCATCGTCTGCTTGGCCCCGGGAGAAGCACTCGGGCCGCCAGGT  
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 GGTGATCATGCGGGACTACCAGCACTTCAACGTGGTGGAGATGTACAAGAGCTACCTGGT  
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 CTACCGAAAGCAGACCTCCACCTGCTGAGCCACCCCCAAGTATGCCTGCCACCTACGCCC  
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 GTATTCTCTCAAAGATTGAAATGTGAAGCCCCAGCCCCACCCTCTGCCCTTCAGCCTAC  
 TGGGCCAGGCCGGACCTGCCCCCTCAGTGTCTCTCCCTCCCGAGTCCCCAGATGGAGACC  
 CCTTTCTACAGGATGACCCCTTGATATTTGCACAGGGATATTTCTAAGAAACGCAGAGGC  
 CAGCGTTCCTGGCCTCTGCAGCCAACACAGTAGAAAAGGCTGCTGTGGTTTTTTAAAGGC  
 AGTTGTCCACTAGTGTCTTAGGCCACTGCAGAGGGCAGACTGCTGGTCTCCACAGATACC  
 TGCTGTTCTCAGCTCCAGCTTCAAACCTCGAGTCTCGAGAGGGCCACGGGGTGGTTTTTA  
 TGACCGGAATCCCGCTTCTCCCTCACGTCTGATGTCCTGAAGGTGCAGTCCCACCTGTA  
 CAGCCCCCTCCCCGCCAAGAACTGTGAATGGCCTGCTCCAGGCCATGGCTGGGGGCAGGGA  
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 CCTCCAGGTCACCCACAGCCAGTTTCAGGAAGGCTGCCCCCTCTCTCCCACTAAGTTCTGG  
 CCTGAAGGGACCTGCTTTCTTGGCCTGGCTTCCACCTCTCCACTCCTGTGTCTACCTGGC  
 CAGTGGAGTGGTCCATGCTAAGTCTAACACTCCTGGGAGCTCAGGAGGCTTCTGAGCTTC  
 TCCTGTACTGTGCATCGTGAGGGCCAGAGACAGGAATGTAAGGATTGGCAACTGTGTTAC  
 CTTTCAAGTTTATCTCAATAACCAGGTCATCAGGGACCCATTGTTCTCTTCAGAACCTTA  
 TCTGGGAGAGAAGGCGAACCACTCCGGGTTTCCATCATGTCAAGGTCACAGGCATCCAT  
 GTGTGCAAACCATCTGCCCCAGCTGCCTCCACAGACTGCTGTCTCCTTGTCTCCTCGGC  
 CCTGCCCCACTTCAGGGCTGCTGTGAGATGGAATTCCAGGAAAGAACTTCAGGTGTCTGG  
 ACCCTTTCTATCTAGATAATAATTTTATAGATTCTTCTGCTCCCTAGTGACCTACCTGGGGG  
 CAAAGAAATTGCAAGGACTTTTTTTTTAAGGGTCAGAGTTTTTCAAAACAAAAGCATCTTCC  
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AGCC

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GGCCAGTGGGGCGAACTGGCAGCTGGCCGGCCCTTTAACACCTACCCGAGGGCTGACAC  
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AGCGGGGGGCTGGCCATCCCCAGTCCTCCTCCTCCTCCTCCCGGCCTCCCACCCGAGC  
CCGAGGTGCCCCCAGCCCTGGAGTGCTGGGACCCCCACGCCTCAGAGCCCCAGCTGGCCCC  
TCCAGCCTGCACCCCCGCCGCCCTGCTGTTCTTGGGCCCCCTGGCCCCCGCTCACCACA  
GCGGGAGCCACAGCGAGTATCCCATGAGCAGTTCCGGGCTGCCCTGCAGCTGGTGGTGGA  
CCCAGGCGACCCCCGCTCCTACCTGGACAACTTCATCAAGATTGGCGAGGGCTCCACGGG  
CATCGTGTGCATCGCCACCGTGCGCAGCTCGGGCAAGCTGGTGGCCGTCAAGAAGATGGA  
CCTGCGCAAGCAGCAGAGGCGCGAGCTGCTCTTCAACGAGGTGGTAATCATGAGGGACTA  
CCAGCACGAGAATGTGGTGGAGATGTACAACAGCTACCTGGTGGGGGACGAGCTCTGGGT  
GGTCATGGAGTTCCTGGAAGGAGGCGCCCTCACCGACATCGTCACCCACACCAGGATGAA  
CGAGGAGCAGATCGCGGCCGTGTGCCTTGCAGTGCTGCAGGCCCTGTGGTGCTCCACGC  
CCAGGGCGTCATCCACCGGGACATCAAGAGCGACTCGATCCTGCTGACCCATGATGGCAG  
GGTGAAGCTGTCAGACTTTGGGTTCTGCGCCCAGGTGAGCAAGGAAGTGCCCCGAAGGAA  
GTCGCTGGTCGGCACGCCCTACTGGATGGCCCCAGAGCTCATCTCCCGCCTTCCCTACGG  
GCCAGAGGTAGACATCTGGTCGCTGGGGATAATGGTGATTGAGATGGTGGACGGAGAGCC  
CCCCTACTTCAACGAGCCACCCCTCAAAGCCATGAAGATGATTCGGGACAACCTGCCACC  
CCGACTGAAGAACCTGCACAAGGTGTCGCCATCCCTGAAGGGCTTCTGGACCGCCTGCT  
GGTGCGAGACCCTGCCCAGCGGGCCACGGCAGCCGAGCTGCTGAAGCACCCATTCTGGC  
CAAGGCAGGGCCGCCTGCCAGCATCGTGCCCTCATGCGCCAGAACCGCACCCAGATGAGG  
CCCAGCGCCCTTCCCCTCAACCAAAGAGCCCCCCCCGGGTACCCCCGCCCCACTGAGGCC  
AGTAGGGGGCCAGGCCTCCCCTCCTCCAGCCCCGGGAGATGCTCCGCGTGGCACCACCC  
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AGAAAAACACAGGGACTCGTGGGAGCAAGCGAGGCTCCCAGGACCCCCACCTCTGGGAC  
AGGCCCTCCCCCATGTTCTTCTGTCTCCAGGAAGGGCAGCGGCCCTCCCATCACTGGAAG  
TCTGCAGTGGGGGTGCTGGGGGTGGAGAGAACTAAGAGGTGAACATGTATGAGTGTG  
TGCACGCGTGTGAGTGTGCATGTGTGTGTGTGTGCAAAGGTCCAGCCACCCCGTCTCCA  
GCCCCGAAGGGGTGTCTGGCGCCTTGCTGACACCCAGCCCCCTCTCCCCCTGAGCCATT  
GTGGGGGTGATCATGAATGTCCGAAGAGTGGCCTTTTCCCGTAGCCCTGCGCCCCCTTT  
CTGTGGCTGGATGGGGAGACAGGTCAGGGCCCCCCCCACCTCTCCAGCCCCCTGCAGCAAT  
GACTACTGCACCTGGACAGCCTCCTCTTTTCTAGAAGTCTATTTATATTGTCATTTTATA  
ACACTCTAGCCCCTGCCCTTATTGGGGGACAGATGGTCCCTGTCTGCGGGGTGGCCCTG  
GCAGAACCACTGCCTGAAGAACCAGGTTCTTGGCCGGTCAGCGCAGCCCCAGCCCGCCCA  
CCCCTGCCTCGAGTTAGTTTTACAATTAACATTGTCTTGTGTTTTGTGAAAAAAAAAAAA  
AAAAAAAAAA

Title: NUCLEIC ACIDS ENCODING  
PAK5 POLYPEPTIDES AND  
METHODS OF USE THEREOF  
Inventor(s): Gregory PLOWMAN et al.  
DOCKET NO.: 034536-1034

**Fig. 9V**  
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>STLK5\_h

MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTFLLQGELHVSKLFNHPNIVPYRATFI  
ADNELWVVTSMAYGSAKDLICTHFMDSGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSNL  
SMISHGQRQRVVHDFPKYSVKVLPWLSPEVLQQLQGYDAKSDIYSVGITACELANGHVPFKDMPATQMLLEKLNGLTGPC  
LLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPSHPHYHRTFSPHFHHFVEQCLQRNPDARPSASTLLNHSF  
FKQIKRRASEALPELLRPVTPITNFEGSQSDHSGIFGLVTNLEEELEVDDWEF

>STLK6\_h

MSLLDCFCTSRTOVESLRPEKQSETSIHQYLVDEPTLSWSRPSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHT  
PTGTLVTIKITNLENCNEERLKAQKAVILSHFFRHPNITTYWTVFTVGSWLWVISPFMAYGSAQQLLRTYFPEGMSETL  
IRNILFGAVRGLNYLHQNCIHRSIKASHILISGDGLVTL SGLSHLSLVKHGQRHRAVDYDFPQFSTSVQPWLSPELLRQ  
51DLHGYNVKS DIYSVGITACELASGQVPFQDMHRTQMLLQKLKPPYSPIDISIFPQSESRMKNSSQSGVDSGIGESVLVSS  
51GTHTVNSDRLHTPSSKTFSPAFFSLVQLCLQQDPEKRPSASSLLSHVFFKQMKESQDSILSLLPPAYNKPSISLPPVLP  
WTEPECDFPDEKDSYWEF

>STLK7\_h

NRDDYELQEVIGSGATAVVQAA YCAPKKEKVAIKRINLEKCKQTSMDLELLKEIQAMSQCHHPNIVSYTTSFVVKDELWLVM  
KLLSGGSVLDIIKHIVAKGEHKS

>ZC4\_h

MAGPGGWRDREVDLGHLPDPTGIFSLDKTIGLGTYGRIYGLGHEKTGAVKVMNARKDEEEDLRTLNLLRKYSFHK  
NIVSYFYGAFKLSPPGQRHQLWMVMELCAAGSVTDVVRMTSNQSLKEDWIAIYICREILQGLAHLHAHRV IHRDIKGNV  
LTHNAEVKLVD FGVSAQVSRINGRRNSFIGTPYWMapeVIDCDEDPRRSYDYRSDVSVGITA IEMAE GAPPLCNLQPLE  
ALFVILRESAPT VKSSGWSRKFFHFM EKCTIKNFLFRPTSANMLQHPFVRDIKNERHVVESLTRHLTGIIKKRQKKEQAR  
EKSKVSTLRQALAKRLSPKRFRAKSSWRPEKLELSDLEARRQRQRWEDIFNQHEEELRQVDKDESSDNDEVFHS

Fig. 10A

IQAEVQIEPLKPYISNPKKIEVQERSPSVPNNQDHAHHVKFSSVPPQRSLLLEQAQKPIDIRQRSSQNRQNWLAAASGDSKH  
KILAGKTQSYCLTIYISEVKKEEFQEGMNQKCQGAQVGLGPEGHCIWQLGESSSEESPTGRRSQSSPPYSTIDQKLLV  
DIHVPDGFVKISPPVYLTNEWVGYNALSEIFRNDWLTAPAVIQPPEEDGDYVELYDASADTDGDDDDDESNDTFEDTYD  
HANGNDDLDNQVDQANDVCKDHDNNKFVDDVNNNYEAPSCPRASYGRDGSCKQDGYDGSRGKEEAYRGYGSHTANRS  
HGGSAASEDNAAIGDQEEHAANIGSERRGSEGGGKGVVRTSEESGALGLNGEENCSETDGPGLKRPASQDFEYLQEEPG  
GGNEASNAIDSGAAPSAPDHESDNKDISESSTQSDFSANHSSPSKSGMSADANFASAILYAGFVEVPEESPQKQSEVNV  
NPLYVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLGTRSNLYLMDRSGKADITKLIRRRPFRQIQVLEPLNLLITISG  
HKNRLRVYHLTWLRNKILNNDPESKRQRQEMLKTEEACKAIDKLTGCEHFSVLQHEETTYIAIALKSSIHLYAWAPK'SFD  
ESTAIVFPTLDHKPVTVDLAIGSEKRLKIFFSSADGYHLIDAESEVMSDVTLPKNPLEIIPQNIILPDCLGIGMMLT  
FNAEALSVEANEQLFKKILEMWKDIPSSIAFECTQRTTGWGQKAEIVRSLSQSRVLESELKRRSICKLRFCLCTRGDKLFFT  
STLRNHHSRVYFMTLGKLEELQSNYDV

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>PAK5\_h

MFGKRKRKREISAPSNFEHRVHTGFDQHEQKFTGLPRQWQSLIEESARRPKPLVDPACITSIQPGAPKTIVRGSKGAKDG  
ALTLLDEFENMSVTRNSLRRDSPPPPARARQENGMPPEEPATTARGGPGKAGSRGRFAGHSEAGGSGDRRRRAGPEKRP  
KSSREGSGGPQESSRDKRPLSGPDVGTQPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIP  
QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPRSPQREPQRVSHEQFRAALQLVDPDGPDRSY  
LDNFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQQRRELLFNEVIMRDYQHENVVEMYNLYLVGDELWVWMEFLEG  
GALTDIVTHTRMNEEQIAAVCLAVLQALSVLHAQGVHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSLVGTPY  
WMAPELISRLPYGPEVDIWSLGIMVIEMVDGEPYPFNEPPLKAMKMIRDNLPPRLKNLHKVSPSLKGFLDRLLVRDPAQR  
ATAAELLKHPFLAKAGPPASIVPLMRQNRT

>GEK2\_h

MAFANFRRIILRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGALAAAKVIETKSEEELEDYIV  
EIEILATCDHPYIVKLLGAYYHDGKLLWIMIEFCPGGAVDAIMLELDRLGLTEPQIQVVCQRMLEALNFLHSKRIIHRDLKA

Fig. 10B

GNVLMTLEGDIRLADFGVSAKNLKTLLQKRDSFIGTPYWMapevVMCETmKdTPYdYKADIwSLGITLIEMaQIEPPHHEL  
NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLEHPFVSSITSNKALRELVAEAKAEVMEEIED  
GRDEGEEDAVDAASTLENHTQNSSEVSPPSLNADKPLEESPSTPLAPSQDSQSVNEPCSPSGDRSLQTTSPPVVAPGN  
ENGLAVPVPLRKSRPVSMdARIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAPGP  
SKRSDCSSLCTSESMDYGTNLSTDLNLNKGMSLSIKDPKLYKKTLLKTRKFVVDGVEVSIITTSKIISEDEKKDEEMRF  
LRRQELRELRLQKEEHRNQTQLSNKHELQLEQMhKRFEQEIINAKKKFFDTELENLERQQKQKQVEKMEQDHAVRRREEAR  
RIRLEQDRDYTRFQEQKLKMKKEVKNEVEKLPRQQRKESMKQKMEEHQTQKKQLLDRDFVAKQKEDLEAMKRLTTDNRRR  
ICDKERECLMKKQELLRDREALWEMEEHQLQERHQLVKQQLKDQYFLQRHELLRKHEKEREQMQRYNQRMIEQLKVRRQQ  
QEKARLPKIQRSEgKTRMAMYKKS LHNGGSAAEQREKIKQFSQQEEKRQKSERLQQQKQHENQMrdMLAQCESNMSEL  
QQLQNEKCHLLVEHETQKLKALDESHNQNLKEWRDKLPRKKALEEDLNQKKREQEMFFKLSEEAECNPSTPSKAAKFF  
PYSSGDAS

Fig. 10C

>STLK5\_h

GGCCAAAGACGGTCGGGGCTTGCTAACTCCAGGAACAGGTTTAAAGTTTTTGAAACTGAAGTAGGTCTACACAGTAGGA  
ACTCATGTCAATTTCTTAAGTAAACAGAGCGAATCAGCGGTCTCGGAAAGTTTCATTGTTGAGGGCTTAAGAG  
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TCTGCCAGAGGGAGGGTGTACGAGCTGCTCACTGTGATAGGCCAAAGGATTTGAGGACCCTGATGACTGTGAATCTAGCAA  
GGTACAAACCAACAGGAGAGTACGTGACTGTACGGAGGATTAAACCTAGAGCTTGTTCCTCAATGAGATGGTAACATTTCTTG  
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GCTGTGGGTGTGCATCATTCATGGCATACGGTTCCTGCAAAAGATCTCATCTGTACACACTTCATGGATGGCATGAATG  
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GTCAAAGCCAGCCACATCCTGATCTCTGTGGATGGGAAGTCTACCTGTCTGGTTTGGCGAGCAACCTCAGCATGATAAG  
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TCCAGCAGAATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACCTGGCCAAACGGC  
CATGTCCCCCTTTAAGGATATGCCCTGCCACCCAGATGCTGTAGAGAACTGAACGGCACAGTGCCCTGCTGTTGGATAC  
CAGCACCATCCCCGCTGAGGAGCTGACCATGAGCCCCCTTCGGCTCAGTGGCCAACTCTGGCCTGAGTGACAGCCTGACCA  
CCAGCACCCCCGGCCCTCCAAACGGTGACTCGCCCTCCACCCCTACCAACCGAACCTTCTCCCCCACTTCCACCACTTT  
GTGGAGCAGTGCCCTCAGCGCAACCCGGATGCCAGGCCCAGTGCCAGCACCTCCTGAACCACTCTTTCTTCAAGCAGAT  
CAAGCGACGTGCCCTCAGAGGCTTTGCCCGAATTGCTTCGTCTGTACCCCCCATCACCAATTTTGAGGGCAGCCAGTCTC  
AGGACCACAGTGGAATCTTTGGCCCTGGTAACAACTGGAAGAGCTGGAGGTGGACGATTGGGAGTTCTGAGCCTCTGCA  
AACTGTGCGCATTTCTCAGCCAGGATGCAGAGGCCACCCAGAGGCCCTTCTCTGAGGGCCGCCACATTCCTCGCCCTCCT  
GGGCAGATTGGGTAGAAAGGACATTTCTCCAGGAAAGTTGACTGCTGACTGATTGGGAAAGAAATCCTGGAGAGATACT  
TCACTGCTCCAAGGCTTTTGAGACACAAAGGGAATCTCAACAACCAAGGATCAGGAGGTCCAAAGCCGACATTCACAGTC  
CTGTGAGCTCAGGTGACCTCTCCGCAAGAGAGAGATGCTGCTCTGGCCCTGGGAGCTGAATTCAGGCCCAGGGTTTGG  
CTCCTTAACCCGAGGACCGCCACCTCTTCCAGTGTCTTGGACCAAGCCCTCATTTCTATTAACTTTTGTCTCTCAGATGCCCT  
CAGATGCTATAGGTCAGTGAAAGGGCAAGTAGTAAGCTGCCCTCCCTTCCCTCAGACCTCTCCCTCATAAATCCAGA  
GAAGGGCATTTCTGCTTTTAAAGCACAGACTAAGGCTGGAAACAGTCCATCTTATCCCTCTTCTGGCTTGGGCCCTGAC

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Fig. 11A

ACCTAAGTCTTTCCACGGTTTATGTGTGCGCTCATTCCTTTCCACCAAGAAATCCATCTTAGCGCCTCCTGCCAGCTG  
CCCTGGTGCTTTCTCCAAGGGCCATCAGTGCTCTTGCCCTAGCTTGAGGGCTTAAGTCCTTATGCTGTGTTAGTTTCGTTGT  
CAGAACAAATTAATAATTTTCAGAGACGCTG

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AAGGAAGATAAAACAAAGCCTTCTTTGGAATAGATGGATTTTGTCACTTCTGTGTGAACATAAAGTGATTCAAATGTCT  
CITTTGGATTGCTTCTGCACCTTCAAGAACACAAAGTTGAATCACTCAGACCTGAAAAACAGTCTGAAACCAAGTATCCATCA  
ATACITGGTGTGATGAGCCAAACCTTTCTCTGGTCACGTCACCTCCACTAGAGCCAGTGAAGTACTATGTTCACCAACGTTT  
CTCACTATGAGCTCCAAGTAGAAATAGGAAGAGGATTTGACAACTTGACITCTGTCCATCTTGCACGGCATACTCCCCACG  
GGAACACTGGTAACATAAAATTAACAATCTGGAAACTGCAATGAAGAACGCCCTGAAAGCTTTACAGAAAGCCGTGAT  
TCTATCCCACTTTTCCGGCATCCCAATATTACAACCTTATTGGACAGTTTTCACCTGTGGCAGCTGGCTTTGGGTTATTT  
CTCCATTTATGGCCTATGGTTCAGCAAGTCAACTCTTGAGGACCTATTTTCTGAAGGAATGAGTGAACTTTAATAAGA  
AACATTCCTTTGGAGCCGTGAGAGGTTGAACCTATCTGCACCAAAATGGCTGTATTCAAGGAGTATTAAAGCCAGCCA  
TATCCTCATTTCTGGTGTGAGGCTAGTGACCTCTCTGGCCCTTCCCATCTGCATAGTTTGGTTAAGCATGGACAGAGGC  
ATAGGGCTGTGTATGATTTCCACAGTTCAGCACATCAGTGCAGCCGTGGCTGAGTCCAGAACTACTGAGACAGGATTTA  
CATGGGTATAATGTGAAGTCAGATATTTACAGTGTGGGATTACAGCATGTGAATTAGCCAGTGGGCAGGTGCCITTCCTCA  
GGACATGCATAGAACTCAGATGCTGTTACAGAAACTGAAAGGTCTCTCTTATAGCCCATTGGATATCAGTATTTTCCCTC  
AATCAGAAATCCAGAAATGAAAAATTTCCAGTCAGGTGAGACTCTGGGATTGGAGAAAGTGTGCTTGTCTCCAGTGGAACT  
CACACAGTAAATAGTGACCGATTACACACACCATCTCTCAAAACCTTCTCTCTGCTTCTTTAGCTTGGTACAGCTCTG  
TTTGCAACAAGATCCTGAGAAAGGCCATCAGCAAGCAGTTTATTGTCCCATGTTTCTTCAACAGATGAAAGAAAGAA  
GCCAGGATTCAATACTTTCACTGTGCTCTCTGCTTATAACAAGCCATCAATATCATTTGCCCTCCAGTGTACCTTGGACT  
GAGCCAGAAATGTGATTTTCTGATGAAAAGACTCATACTGGGAATTTCTAGGGCTGCCAAATCATTTTATGTCTCTATA  
CTTGACACTTTCTCTGCTGCTTTTCTCTGTATTTCTAGGTACAAATACCAGAAATTATACTTGAATAACAGTTGGT  
GCACCTGGAGAACTCTATTATTTAAACCCACTCTGTTCAAAAGGGGCACCCAGTTTGTAGTCCCTCTGTTTCGCACAGAGTACT  
ATGACAAGGAAACATCAGAAATTACTAATCTAGCTAGTGTCAATTTATCTGGAAATTTTCTTAAGCTGTGACTAATCT

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Fig. 11B

TTTATCTCTCAATATAATTTTGGAGCCAGTTAAATTTTTCAGTATTTTGTCTGTCCTTGGGAATGGGCCCTCAGAGGAC  
AGTGCTTCCAAAGTACATCTTCTCCAGATCTCTGGCCCTTTTAAATGAGCTATTTGTTAAACCAACAGGCTAGTTTATCTT  
ACATCAGACCCCTTTTCTGGTAGAGGGGAAAATGTTTGTGCTTTTCCCTTTTCTTCTGTAACTTATGGTAAACACCTAAC  
TGAGCCCTCACTCACATTAAATGATTCACTTGAAATATATACAGAAAATGTAAATTTGCTTTTAAAAAAGGGGCTAA  
AGTAACACTTTCTACTTATGTAAATTATAGATCTCTAAATTCACGCCACCCCGTGGGAGCTCAATAAAGATTTACTGAATT

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TCAACAGGGACGATTACGAGCTGCAGGAGGTGATCGGGAGTGGAGCAACTGCTGTAGTCCAAAGCAGCTTATTGTGCCCT  
AAAAGGAGAAAAGTGGCAATCAAAACGGATAAACCTTGAGAAAATGTCAAACTAGCATGGATGAACTCTGAAAAGAAATTCA  
AGCCATGAGTCAATGCCATCATCCTAATAATTGTATCTTACTACACATCTTTTGTGGTAAAGATGAGCTGTGGCTTGTCA  
TGAAAGCTGCTAAGTGGAGGTTCTGTCTGGATATTAAGCACATTTGTGGCAAAAGGGGAACACAAAAGT

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ATGGCGGGACCTGGGGGCTGGAGGGACAGGGAGGTACGGGATCTGGGCCACCTGCCGGATCCAACTGGAATATTCTCACT  
AGATAAAACCATTTGGCCTTGGTACTTATGGCAGAACTCTATTTGGGACTTCATGAGAAAGACTGGTGCAATTACAGCTGTTA  
AAGTGATGAACGCTCGTAAGGATGAGGAAGGATCTCAGGACTGAACCTCAACCTTCTGAGGAAGTACTCTTTCCACAAA  
AACATTGTGTCCTTCTATGGAGCAATTTTCAAGCTGAGTCCCCCTGGTCAGCGGCCAACCTTTGGATGGTGATGGAGTT  
ATGTGCAGCAGGTTCCGTCACCTGATGTAGTGAGAAATGACCAGTAATCAGAGTTTAAAGAAGATTGGATTGCTTATATCT  
GCCGAGAAAATCCTTCAGGGCTTAGCTCACCTTCACGCCACACCGAGTAATTCACCGGGACATCAAGGTCAGAAATGTGCTG  
CTGACTCATAAATGCTGAAGTAAACTGGTTGATTTTGGAGTGAGTGCCTCAGGTGAGCAGAACTAATGGAAGAAGGAATAG  
TTTCATTGGGACACCATACTGGATGGCACCTGAGGCTGATTGACTGTGATGAGGACCCCAAGACGCTCCTATGATTACAGAA  
GTGATGTGTGCTGTGGGAATTACTGCCCATTTGAAATGGCTGAAGGAGCCCTCTCTGTGTAACTTCAACCTTTGGAA  
GCTCTCTTCGTTATTTTGGCGGAACTCTGCTCCACAGTCAAAATCCAGCGGATGGTCCCGTAAGTTCACAAATTTTCATGGA  
AAAGTGACGATAAAAAATTTCTGTTCTGTCCTACTTCTGCAAAACATGCTTCAACACCCCATTTGTCGGGATATAAAAA

Fig. 11C



**Fig. 11D**

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**Fig. 11E**

GAGGTGCCCCAGCCCTGGAGTGTGGGACCCACGCTCAGAGCCCCAGCTGGCCCCCTCCAGCCCTGCACCCCCCGCCGCC  
CCTGCTGTTCCCTGGGCCCCCTGGCCCTCACACAGCGGGAGCCACAGCGAGTATCCCATGAGCAGTTCCGGGCTGC  
CCTGCAGCTGGTGGACCCAGGCGACCCCGCTCCCTACCTGGACAACCTCATCAAGATTGGCGAGGGCTCCACGGGCA  
TCGTGTGCATCGCCACCGTGGCAGCTCGGGCAAGCTGGTGGCCGTCAAGAAAGATGGACCTGCGCAAGCAGCAGAGGCGC  
GAGCTGCTCTTCAACGAGGTGGTAATCATGAGGGACTACACGACGAGAAATGTGGTGGAGATGTACAACAGCTACCTGGT  
GGGGACGAGCTCTGGGTGGTCAATGGAGTTCCTGGAAAGGAGGCCCTCACCGACATCGTCACCCACACAGGATGAACG  
AGGAGCAGATCGGGCCGTGTGCTGAGTGTGAGGCCCTGTGCTCCACGCCAGGGCGTCAATCCACCGGGAC  
ATCAAGAGCGACTCGATCCTGCTGACCCATGATGGCAGGGTGAAGCTGTAGACTTTGGGTTCTGGCCCCAGGTGAGCAA  
GGAAGTCCCCGAAGGAGTCTGGTCGGCACGCCCTACTGGAATGGCCCCAGAGCTCATCTCCGCTTCCCTACGGGC  
CAGAGGTAGACATCTGGTCTGGGGATAATGGTGAATGAGATGGTGGACGGAGAGCCCCCTACTTCAACGAGCCACCC  
CTCAAAGCCATGAAGATGATTCTGGGACAACTGCCCCAGCTGAAGAACCTGCACAAAGGTGTGCGCATCCCTGAAGGG  
CTTCTCTGACCCGCTGTGTCGGAGACCTGCCCCAGCGGGCCACGGCAGCTGCTGAAGCACCCATTCCTGGCCA  
AGGAGGGCCGCTGCCAGCATCGTGCCCCCTCATGCGCCAGAACCGCACCATGAGGCCAGCGCCCTTCCCTCAACC  
AAAGAGCCCCCGGGTCAACCCCGCCCACTGAGGCCAGTAGGGGCCAGGCCCTCCACTCTCCAGCCCCGGGAGATG  
CTCCGCTGGCACCCCTCTTGTGGGGTAGATGAGACCTACTGAACTCCAGTTTGTATCTCGTGACTTTTAG  
AAAAACAGGGACTCGTGGGAGCAAGCAGGCTCCAGGACCCCACTCTGGGACAGGCCCTCCCCCATGTTCTCT  
GTCTCCAGGAAGGCGCCCTCCCATCACTGGAAGTCTGCAGTGGGGTCTGCTGGGGTGGAGAGACACTAAGAGG  
TGAACATGTATGAGTGTGCACGCGTGTGAGTGTGATGTGTGTGTGCAAGGTCCAGCCACCCGCTCCAGC  
CCGCAAGGGGTGTCTGGCGCTTGCCCTGACACCCAGCCCCCTCTCCCCCTGAGCCATTTGTGGGGTGCATCATGATGTC  
CGAAGAGTGGCCCTTTTCCCGTAGCCCTGCGCCCCCTTCTGTGGCTGGAATGGGGAGACAGGTCAAGGCCCTCCACCTCT  
CCAGCCCCCTGCAGCAAAATGACTACTGCACCTGGACAGCCCTCTCTTTCTAGAACTCTATTTATATTGTCAATTTATAC  
ACTCTAGCCCCCTGCCCTTATTGGGGGACAGATGGTCCCTGTCTGCGGGGTGGCCCTGGCAGAACCACTGCTGAAGAAC  
CAGGTTCTGCCCCGGTCAAGCGCAGCCCCAGCCCCACCCCTGCTCGAGTTAGTTTACAAATTAACAATTGTCTTGT  
TTTGTG

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CGAAGCCACAGCCCGAGCCCGAGCCCGGCGCCACCGCGCCCCCGGCCCATGGCTTTTGGCCAATTTCCGGCC  
GCATCCTGCGCCTGTCTACCTTCGAGAAAGAGAAAGTCCCGCGAATAATGAGCACGTCCGCGCGGACCTGGACCCCAACGAG  
GTGTGGGAGATCGTGGCGGAGCTGGCGGACGCGCCCTTCGGCAAGGTTTACAAGGCCAAGAAATAAGGAGACGGGTGCTTT  
GGCTGGCGGCCAAAGTCAATTGAACCAAGAGTGAGGAGGAGCTGGAGGACTACATCGTGGAGATTGAGATCCTGGCCACCT  
GGGACCAACCCCTACATTGTGAAGCTCCTGGGAGCCTACTATCACGACGGGAAGCTGTGGATCATGATTGAGTTCTGTCCA  
GGGGAGCCGTGGACGCCATCATGTCTGGAGCTGGACAGAGGCCCTCACGGAGCCCCAGATACAGGTGGTTTGGCGCCAGAT  
GCTAGAACCCCTCAACTTCCTGCACAGCAAGAGGATCATCCACCGAGATCTGAAGCTGGCAACGTGCTGATGACCCCTCG  
AGGGAGACATCAGGCTGGCTGACTTTGGTGTCTGTGCCAAGAACTGAAGACTTACAGAAACGAGATTCTTTCATCGGC  
ACGCCTTACTGGATGGCCCCCGAGGTGGTCAATGTGTGAGACCATGAAGACACGCCCTACGACTACAAAGCCGACATCTG  
GTCCCTGGGCATCACGCTGATTGAGATGGCCCCAGATCGAGCCGCCACACACGAGCTCAACCCCATGCGGGTCTCTGCTAA  
AGATCGCCAAAGTCGGACCCCTCCACGCTGCTCACGCCCTCCAAAGTGGTCTGTAGAGTTCCGTGACTTCTTGAAGATAGCC  
CTGGATAAGAACCCAGAACCCGACCCAGTGGCCGCGAGCTGCTGGAGCATCCCTTCGTGAGCAGCATCACCAAGTAACAA  
GGCTCTGCGGGAGCTGGTGGCTGAGGCCAAGGCCGAGGTGATGGAAGAGATCGAAGACGGCCGGGATGAGGGGGAAAGAGG  
AGGACGCCGTGGATGCCGCCCTCCACCCCTGGAGAACCATACTCAGAACTCCTCTGAGGTGAGTCCGCCAAGCCTCAATGCT  
GACAGCCTCTCGAGGAGTCACTTCCACCCCGCTGGCACCCAGCCAGTCTCAGGACAGTGTGAATGAGCCCTGCAGCCA  
GCCCTCTGGGGACAGATCCCTCCAAACCAACCACTCCAGTCCCCAGTCCGTGGCCCCCTGGAAATGAGAACGGCCTGGCAGTGCCTG  
TGCCCCCTGGGGAAGTCCCGACCCGTGTCAATGGATGCCAGAAATTCAGGTAGCCCAAGGAGAACAGTTGCTGAGCAGGGT  
GGGGACCTCAGCCAGCAGCCAAACAGATCTCAAAGGCCAGCCAGAGCCGCCCAACAGCAGCGCCCTGGAGACCTTGGG  
TGGGGAGAAAGCTGGCCCAATGGCAGCCTGGAGCCACCTGGCCAGGCAGCTCCAGGGCCTTCCAAGAGGACTCGGACTGCA  
GCAGCCTCTGCACCTCTGAGAGCATGGACTATGGTACCAATCTCTCCACTGACCTGTCTGCTGAACAAGAGATGGGCTCT  
CTGTCCATCAAGGACCCGAAACTGTACAAAACCCCTCAAGCGGACACGCAAAATTTGTGGTGGATGGTGTGGAGGTGAG  
CATCACCACTCCAAGATCATCAGCGAAGATGAGAAGAAAGGATGAGGAGATGAGATTCTCAGGGCCCAAGAACTCCGAG  
AGCTTCGGCTGCTCCAGAAAGAGAGCATCGGAACCAAGACCCAGCTGAGTAACAAGCATGAGCTGCAGCTGGAGCAAAATG  
CATAAACGTTTTGAACAGGAAATCAACGCCCAAGAAAGATTCTTTGACACGGAAATTAGAGAACCTGGAGCGTCAAGCAAA

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Fig. 11G

GCAGCAAGTGGAGAAGATGGAGCAAGACCATGCCGTCGCCGCCGGGAGGAGGCCAGGGCGGATCCGCCCTGGAGCAGGATC  
GGGACTACACCAGGTTCCAAAGAGCAGCTCAAACTGATGAAGAAAGAGGTGAAGAACGAGGTGGAGAAAGCTCCCCGACAG  
CAGCGGAAGAAAGCATGAAGCAGAAAGATGGAGGAGCACACGCAAGAAAGCAGCTTCTTGACCCGGGACTTTGTAGCCAA  
GCAGAAAGGAGGACCTGGAGCTGGCCATGAAGAGGCTACCAACGACAAACAGCGGGGAGATCTGTGACAAAGGAGCGCGAGT  
GCCCTCATGAAGAAAGCAGGAGCTCCTTCGAGACCGGGAAGCAGCCCTGTGGGAGATGGAAAGACCAAGCTGCAGGAGAGG  
CACCAAGCTGGTGAAGCAGCAGCTCAAAGACCAGTACTTCCTCCAGCGGCACGAGCTGCTGCCAAGCATGAGAAGGAGCG  
GGAGCAGATGCAGCGCTACAACAGCGCATGATAGAGCAGCTGAAGGTGCGGCAGCAACAGGAAAGGCGGCTGCCCA  
AGATCCAGAGGAGTGAGGGCAAGACGCGCATGGCCATGTACAAGAAAGAGCTCCACATCAACGGCGGGGCGAGCGCA'GCT  
GAGCAGCGTGAGAAGATCAAGCAGTTCTCCAGCAGGAGGAGAAAGAGGCGGCTGCGAGCGGCTGCAGCAACAGCAGAA  
ACACGAGAACCCAGATGCGGGACATGCTGGCGCAGTGCGGAGCAACATGAGCGAGCTGCAGCAGCTGCAGAAATGAAAAGT  
GCCACCTCCTGTAGACACGAAACCCAGAACTGAAGGCCCTGGATGAGAGCCATAACCAAGAACCTGAAGGAATGGCGG  
GACAAAGCTTCGGCCCGCAAGAGGCTCTGGAAGAGGATCTGAACCAAGAAAGCGGGAGCAGGAGATGTTCTTCAAGCT  
GAGCGAGGAGGCGGAGTGCCCCAACCCCTCCACCCCAAGCAAGGCCCAAGTTCTTCCCCCTACAGCTCTGGGGATGCTT  
CC

Fig. 11H

STLK6_h	-----MSL	L	D	C	F	C	T	S	R	T	Q	V	E	S	L	R	P	E	K	Q	S	E	T	S	I	H	Q	Y	L	V	D	E	P	T	L	S	W	S	R	41												
STLK5_h	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	0													
SPAK_h	MAEP	S	G	S	P	V	H	V	Q	L	P	Q	A	A	P	V	T	A	A	A	A	A	P	A	A	T	A	A	P	A	A	P	A	A	P	A	P	A	P	A	50											
STLK6_h	P	S	T	R	A	S	E	-	V	L	C	S	T	N	V	S	H	Y	E	L	Q	V	E	I	G	R	G	F	D	N	L	T	S	V	H	L	A	R	H	T	P	T	G	T	L	V	T	I	K	I	90	
STLK5_h	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	9		
SPAK_h	P	A	A	Q	A	V	G	W	P	I	C	R	D	A	-----	Y	E	L	Q	E	V	I	G	S	G	A	T	A	V	-----	V	Q	A	A	L	C	K	P	R	Q	E	R	V	A	I	K	R	95				
STLK7_h	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	N	R	D	D	Y	E	L	Q	E	V	I	G	S	G	A	T	A	V	-----	V	Q	A	A	Y	C	A	P	K	K	E	K	V	A	I	K	R	35
STLK6_h	T	N	L	E	N	C	N	E	E	R	L	K	A	L	Q	K	A	V	I	L	S	H	F	F	R	H	P	N	I	T	T	Y	W	T	V	F	T	V	G	S	W	L	W	V	I	S	P	F	M	A	140	
STLK5_h	I	N	L	E	A	C	S	N	E	M	V	T	S	-	C	R	A	S	C	M	F	Q	T	L	N	H	P	N	I	V	P	Y	R	A	T	L	I	A	D	N	E	L	W	V	V	T	S	F	M	A	58	
SPAK_h	I	N	L	E	K	C	Q	T	S	M	D	E	L	L	K	E	I	Q	A	M	S	Q	C	-	S	H	P	N	V	V	T	Y	T	S	F	V	V	K	D	E	L	W	L	V	M	K	L	L	S	144		
STLK7_h	I	N	L	E	K	C	Q	T	S	M	D	E	L	L	K	E	I	Q	A	M	S	Q	C	-	H	H	P	N	I	V	S	Y	T	S	F	V	V	K	D	E	L	W	L	V	M	K	L	L	S	84		
STLK6_h	Y	G	S	A	S	Q	L	L	R	T	Y	F	P	E	G	-----	M	S	E	T	L	I	R	N	I	L	F	G	A	V	R	G	L	N	Y	L	H	Q	N	G	C	I	H	R	S	184						
STLK5_h	Y	G	S	A	K	D	L	I	C	T	H	F	M	D	G	-----	M	N	E	L	A	I	A	Y	I	L	Q	G	V	L	K	A	L	D	Y	I	H	M	G	Y	V	H	R	S	102							
SPAK_h	G	G	S	M	L	D	I	I	K	Y	I	V	N	R	G	E	H	K	N	G	V	L	E	E	A	I	A	T	I	L	K	E	V	L	E	G	L	D	Y	L	H	R	N	G	Q	I	H	R	D	194		
STLK7_h	G	G	S	V	L	D	I	I	K	H	I	V	A	K	G	E	H	K	S	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	103			
STLK6_h	I	K	A	S	H	I	L	I	S	G	D	G	L	V	T	L	S	G	L	S	H	L	H	S	L	V	K	H	G	Q	-----	R	H	R	A	V	Y	D	F	P	Q	F	S	T	S	V	Q	P	W	232		
STLK5_h	V	K	A	S	H	I	L	I	S	V	D	G	K	V	Y	L	S	G	L	R	S	N	L	S	M	I	S	H	G	Q	-----	R	Q	R	V	V	H	D	F	P	K	Y	S	V	K	V	L	P	W	150		
SPAK_h	L	K	A	G	N	I	L	L	G	E	D	G	S	V	Q	I	A	D	F	G	V	S	A	F	L	A	T	G	G	D	V	T	R	N	K	V	R	K	T	F	-----	V	G	T	P	C	W	240				

Fig. 12A

**Fig. 12B**

PAK1_h U51120	MSNNGLDIQDKPPAPPMRNTSTMIGAGSKDAGTLNHGSKPLPPNPEEKKKKDRFYRSILP	60
PAK4_h	-----	0
PAK5_h	-----	0
PAK1_h U51120	GDKTNKKKEKERPEISLPSDFEHTIHVGFDAVT-GEFTGMPEQWARLQTSNITKIS---	115
PAK4_h	---MFRKKKKRPEISAPQNFQHRVHTSFDPKEGKFVGLPPQWQNILD-ILRRPKPVVDP	56
PAK5_h	---MF-GKRKKRVIEISAPSNFEHRVHTGFDQHEQKFTGLPRQWQSLIEESARRPKPLVDP	56
PAK1_h U51120	-----	115
PAK4_h	SRITRVQLQPMKTVVRGSAAMPVDGYTSGLLNDITQKLSVISNTLRGRSPTSRRAQLSLGL	116
PAK5_h	ACITSIQPGAPKTIVRGSKGAKDGAITLLDDEFENMSVTRSNGLRRDSPPPARAR---	112
PAK1_h U51120	-----	115
PAK4_h	LGDEHWATDPDMYLQSPQSERTDPHGLYLSGNGGTPAGHKQMPWPEPQSPRVLNGLAAK	176
PAK5_h	-----QENGMPPEPATTAARGGPK	131
PAK1_h U51120	-----	127
PAK4_h	AQSLGPAEFQGAQRCLQLGACLQSSPPGASPPPTGTNRHGMKA AKHGSEEARPQSCLVGS	236
PAK5_h	AGSRGR---FAGHSEAGGSGDRRRAAGPEKRPKSSREGSGGPGQESSRDKRP---LSGP	183
PAK1_h U51120	LEFY-N SKKT SN SQKYMSFTDKS-----AEDYNSSNALNVKA-----VSETPAVPPVS	174
PAK4_h	ATGRPGGEGSPSPKTRESSLKRLFRSMFLSTAAITAPSSSKPPGPVPPQSKPNSSFRPPQK	296
PAK5_h	DVGTPOPAAGLASGAKLAAG-----RPFNTYPRADTDHPSTRCAQGEPHDVAPNGP-----	232

Fig. 13A



PAK1_h U51120	E	E	D	E	D	D	D	D	A	T	P	P	P	V	I	A	P	R	P	E	H	T	K	S	V	T	R	S	-	-	-	-	V	I	E	P	L	P	V	I	P	T	R	D	V	A	T	S	P	I	S	P	T	E	N	N	T	I	T	230		
PAK4_h	D	N	P	P	S	L	V	A	K	A	Q	S	L	P	S	D	Q	P	V	G	T	F	S	P	L	T	S	D	T	S	S	P	Q	K	S	L	R	T	A	P	A	T	G	Q	L	P	G	R	S	S	P	A	G	S	P	R	T	W	H	356		
PAK5_h	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	A	G	G	L	A	I	P	O	S	S	S	S	S	R	P	T	R	A	R	G	A	P	S	P	G	V	L	-	-	-	-	-	-	-	-	-	G	P	H	A	S	E	268	
PAK1_h U51120	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	D	A	L	T	L	N	T	E	K	Q	K	K	P	K	M	S	D	E	E	I	L	E	K	L	R	S	I	V	S	G	D	P	K	K	K	Y	T	R	F	E	K	I	276	
PAK4_h	A	Q	I	S	T	S	N	L	Y	L	P	Q	D	P	T	V	A	K	G	A	-	-	-	L	A	G	E	D	T	G	V	V	T	H	E	Q	F	K	A	L	R	M	V	V	D	Q	G	D	P	R	L	L	D	S	Y	V	K	I	413			
PAK5_h	P	Q	L	A	P	P	A	-	C	T	P	A	A	V	P	G	P	P	R	S	P	Q	R	E	P	D	R	V	S	H	E	Q	F	R	A	L	Q	L	V	V	D	P	G	D	P	R	S	Y	L	D	N	F	I	K	I	327						
PAK1_h U51120	G	Q	G	A	S	G	T	V	Y	T	A	M	D	V	A	T	G	Q	E	V	A	T	K	Q	M	N	L	Q	Q	Q	P	K	K	E	L	I	T	N	E	I	L	V	M	R	E	N	K	N	P	N	I	V	N	Y	L	D	S	Y	L	V	336	
PAK4_h	G	E	G	S	T	G	I	V	C	L	A	R	E	K	H	S	G	R	Q	V	A	V	K	M	M	D	L	R	K	Q	Q	R	R	E	L	L	F	N	E	V	V	I	M	R	D	Y	Q	H	E	N	V	V	E	M	Y	K	S	Y	L	V	473	
PAK5_h	G	E	G	S	T	G	I	V	C	I	A	T	V	R	S	S	G	K	L	V	A	V	K	K	M	D	L	R	K	Q	Q	R	R	E	L	L	F	N	E	V	V	I	M	R	D	Y	Q	H	E	N	V	V	E	M	Y	N	S	Y	L	V	387	
PAK1_h U51120	G	D	E	L	W	V	V	M	E	Y	L	A	G	G	S	L	T	D	V	V	T	E	T	C	M	D	E	G	Q	I	A	A	V	C	R	E	C	L	Q	A	L	E	S	L	H	S	N	Q	V	I	H	R	D	I	K	S	D	N	I	L	396	
PAK4_h	G	E	E	L	W	V	L	M	E	F	L	Q	G	G	A	L	T	D	I	V	S	Q	V	R	L	N	E	E	Q	I	A	T	V	C	E	A	V	L	Q	A	L	A	Y	L	H	A	Q	G	V	I	H	R	D	I	K	S	D	S	I	L	533	
PAK5_h	G	D	E	L	W	V	V	M	E	F	L	E	G	G	A	L	T	D	I	V	T	H	T	R	M	N	E	E	Q	I	A	A	V	C	L	A	V	L	Q	A	L	S	V	L	H	A	Q	G	V	I	H	R	D	I	K	S	D	S	I	L	447	
PAK1_h U51120	L	G	M	D	G	S	V	K	L	T	D	F	G	F	C	A	Q	I	T	P	E	Q	S	K	R	S	T	M	V	G	T	P	Y	W	M	A	P	E	V	T	R	K	A	Y	G	P	K	V	D	I	W	S	L	G	I	M	A	I	E	456		
PAK4_h	L	T	L	D	G	R	V	K	L	S	D	F	G	F	C	A	Q	I	S	K	D	V	P	K	R	K	S	L	V	G	T	P	Y	W	M	A	P	E	V	I	S	R	S	L	Y	A	T	E	V	D	I	W	S	L	G	I	M	V	I	E	593	
PAK5_h	L	T	H	D	G	R	V	K	L	S	D	F	G	F	C	A	Q	I	V	S	K	E	V	P	R	R	K	S	L	V	G	T	P	Y	W	M	A	P	E	L	I	S	R	L	P	Y	G	P	E	V	D	I	W	S	L	G	I	M	V	I	E	507
PAK1_h U51120	M	I	E	G	E	P	P	Y	L	N	E	N	P	L	R	A	L	Y	L	I	A	T	N	G	T	P	E	L	Q	N	P	E	K	L	S	A	I	F	R	D	F	L	N	R	C	L	E	M	D	V	E	K	R	G	S	A	K	E	L	L	516	
PAK4_h	M	V	D	G	E	P	P	Y	F	S	D	S	P	V	Q	A	M	K	R	L	R	D	S	P	P	K	L	K	N	S	H	K	V	S	P	V	L	R	D	F	L	E	R	M	L	V	R	D	P	Q	E	R	A	T	A	Q	E	L	L	653		
PAK5_h	M	V	D	G	E	P	P	Y	F	N	E	P	L	K	A	M	K	M	I	R	D	N	L	P	P	R	L	K	N	L	H	K	V	S	P	S	L	K	G	F	L	D	R	L	L	V	R	D	P	A	Q	R	A	T	A	A	E	L	L	567		

Fig. 13B

545  
 681  
 591

PAK1_h	U51120	Q	H	Q	F	L	K	I	A	K	P	L	S	L	T	P	L	I	A	A	K	E	A	T	K	N	N	H	
PAK4_h		D	H	P	F	L	I	Q	T	G	L	P	E	C	L	V	P	L	I	Q	L	Y	R	K	Q	T	S	T	C
PAK5_h		K	H	P	F	L	A	K	A	G	P	P	A	S	I	V	P	L	M	R	Q	N	R	I	R				



-  RESIDUES THAT MATCH THE CONSENSUS NAMED CONSENSUS #1 EXACTLY.
-  BOX RESIDUES THAT MATCH THE CONSENSUS EXACTLY.

Fig. 13C

ZC4_h.pro	MAGPGGWRDREVTDLGHLPDPTGIFSLDKTIIGLGTYGRIYLGHEKGTGAF	50
ZC1_h.pro	MANDSPAKSLVDIDLSSLRDPAGIEELVEVVGNGTYGQVYKGRHVKTGQL	50
ZC4_h.pro	TAVKVMNARKDEEEDLRTIELNLLRKYSFHKNTVSFYGAFFKLSPPGGRHQ	100
ZC1_h.pro	AAIKVMDVTEDEEEFIKLEINMLKKYSHHRNIAITYYGAFIKKSPPGHDDQ	100
ZC4_h.pro	LWMVME LCAAGSVTDVVRMTSNQSLKEDWIAIYICREILQGLAHLHAHRVI	150
ZC1_h.pro	LWLVMEFCGAGSITDLVKNTKGNLTLEDWIAIYSREILRGLAHLHIHVI	150
ZC4_h.pro	HRDIKGQNVLLTHNAEVKLVDFGVSAQVSRITNGRRNSFIGTPTYWMAPEVI	200
ZC1_h.pro	HRDIKGQNVLLTENA EVKLVDFGVSAQLDRITVGRRTFIGTPTYWMAPEVI	200
ZC4_h.pro	DCDEDPRRSYDYRSVSVGITAITEMAEGAPPLCNLQPLEALFYILRESA	250
ZC1_h.pro	ACDENPDATYDYRSDLWSGCGITAIEMAEGAPPLCDMHPMRALFLIPRNP	250
ZC4_h.pro	PTVKSSGWSRKFFHNFMEKCTIKNFLFRPTSANMLQHPFVRDIKNERHVVE	300
ZC1_h.pro	PRLKSKKWSKKFFSFTIEGCLVKNYMQRPSTEQLLKHPIRDQPNRQVRI	300
ZC4_h.pro	SLTRHLTGIKKR-----OKKEQAREKKS	324
ZC1_h.pro	QLKDHIDRTRKRRGEKDETEYEYSGSEEEEEVEPEGEPESSIVNVPGES	350
ZC4_h.pro	KVSTLRQALAKRLSPKKRFRRAKSSWRPEKLELSDLEARRQRRQRWEDIFN	374
ZC1_h.pro	TLRRDFLRLLQQENKERSEALRRRQQLLQEQQLREQEEYKRQLLAERQKRIE	400
ZC4_h.pro	QHEEELRQVDKDKEDSSNDDEVFHSIOAEVQTEPLKPYISNPKKIEVQE	424
ZC1_h.pro	QQKEQRRRLLEEQQRREREARRQQREREQRRREQEEKRRRLEELERRRKEEEE	450

Fig. 14A

ZC4_h.pro	RSPVPPNNQDHAHHVKFFSSVPQRSLLLEQAQKPIDIRQRSSQNRQNWLA	474
ZC1_h.pro	RRRAEEKRRVEREREQEIYIRRRQLEEEQRHLEVLQQQLLEQAMLLLECRWRE	500
ZC4_h.pro	SGDSKHKILAGKTQSYCLTIYIYISEVKKKEEFQEGMNQKCCQAQVGLGPEGH	524
ZC1_h.pro	MEEHRQAERLQRQLQQEQAYLLSLQHDHRRPHPHQHSQQPPPPQQRSKPS	550
ZC4_h.pro	CIWQLGESSSEEEESPVTGRRSQSSPPYSTIDQKLLVDIHVPDGFVKVGI	574
ZC1_h.pro	FHAPEPKAHYEPADRAREVEDRFRKTNHSSPEAQSKQTGRVLEPPVPSRS	600
ZC4_h.pro	PPVYLTNEWVGYNALSEIFRNDWLTIPAVIOPPEEDGDYVELYDASADTD	624
ZC1_h.pro	ESFSNGNSESVHPALQRPAPQVPVRTTSRSPVLSRRDSPLQGSQQNSQ	650
ZC4_h.pro	GDDDESNDFEEDTYDHANGNDLDNQVDQANDVCKDHDNDNNKFVDDVN	674
ZC1_h.pro	AGQRNSTSIEPRLLWERVEKLVPRPGSSSSGSSNSGSPGSHPGSGSGS	700
ZC4_h.pro	NNYYEAPSCPRASYGRDGSCKQDGYDGGSRGKEEAYRGYGSHTANRSHGGS	724
ZC1_h.pro	GERFRVRSSSKSEGPSQRLENNAVKKPEDKKEVFRPLKPADLTALAKELR	750
ZC4_h.pro	AASEDNAATGDOEEHAANIGSERRGSEGDGGKGVVRTSEESGALGLNGEE	774
ZC1_h.pro	AVEDVRPPHKVTDYSSSEESGTTDEEDDVEQEGADESTSGPEDTRAAS	800
ZC4_h.pro	NCSETDGPGLKRPASQDFFEYVLOEEPPGGGNEASNAIDSGAAPSA PDHESDN	824
ZC1_h.pro	SLNLSNGETESVKTMIVHDDVESEPIAMTPSKEGTLIVRRRTQSA SSTLQKH	850
ZC4_h.pro	KDISESSSTOSDFSANHSSPSKSGSGMSADANFASAILYAGFVEVPEESP	874
ZC1_h.pro	KSSSFTFPFIDPRLLQISPSGTTVTTSVVGESCDGMRPE--AIRQDPTRK	898

Fig. 14B

ZC4_h.pro	PSEVNVNPLYVSPACKKPLIHMYEKEFTSEICGSLWGVNLLLGTRSNLY	924
ZC1_h.pro	GSVVNVNPTNTRPQSDTPEIRKYKKRFNFSEILCAALWGVNLLVGTESGLM	948
ZC4_h.pro	LMDRSGKADITKLIIRRRPFRQIQVLEPLNLLITISGHNKRLRVYHLLTWLR	974
ZC1_h.pro	LLDRSGQGKVPYPLINRRRFQIQMDVLEGLNVLLVITISGKKDKLRYVYLLSWLR	998
ZC4_h.pro	NKILNNDPESKRRQE-EMLKTEEACKAIDKLTGCEHFSVLQHEETIYIAI	1023
ZC1_h.pro	NKILHNDPEVEKKQGW-TVGDLFGCVHYKVVKYERIKFLVI	1039
ZC4_h.pro	ALKSSIHLAYAWAPKSFDESTAIKVFPITLDHKPVTVDLAIGSEKRLKIFFS	1073
ZC1_h.pro	ALKSSVEVYAWAPKPYHKFMAFKSEFGEIVHKKPLLVDLITVEEGQRLKVIYG	1089
ZC4_h.pro	SADGYHLIDAESEVMSDVTLPKNPLEIIPQNIILPDCLGIGMMILTFNA	1123
ZC1_h.pro	SACGFHADVDSGSVYDIYLPHTHIQCSIKPHAIIILPNTDGMELLVCYED	1139
ZC4_h.pro	EALSVANEQLFKKILEMWKDIPSSIAFECTORITGWGOKAIEVRSLSQSR	1173
ZC1_h.pro	EGVYVNTYGRITKDVVLQWGMPTSVAYIRSNQIMGWGEKAIETRSVETG	1189
ZC4_h.pro	VLESELKRRSIIKKLRFCLCTRGDKLFFFTSLRNHHSRVYFMTLGKLEELQS	1223
ZC1_h.pro	HLDGVFMHKRAQRLLKFLCERNDKVFFASVRS GGSSQVYFMTLGR TSLLSW	1239
ZC4_h.pro	NYDV	1227
ZC1_h.pro		1239

BOX RESIDUES THAT MATCH ZC4\_h.pro EXACTLY.

Fig. 14C

Db = LOK1\_m

Qy = GEK2\_h

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*****
*****
Db 1 1MAFANFRRI LRLSTFEKRKSREYEHVRRDLDPNDVWEIVGELGDGAFGKVYKAKNKETGA 60
Qy 1 1MAFANFRRI LRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGA 60

*****
*****
Db 61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYDGGKLIWIMIEFCPGGAVDA 120
Qy 61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLIWIMIEFCPGGAVDA 120

*****
*****
Db 121 IMLELDRGLTEPQIQVVCQRMLEALNFLHGKRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180
Qy 121 IMLELDRGLTEPQIQVVCQRMLEALNFLHRSKRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180

*****
*****
Db 181 KNLKTLLQKRDSFIGTPYWMAPPEVVLCEETMKDAPYDYKADIWSLGITLIEMAQIEPPHHEL 240
Qy 181 KNLKTLLQKRDSFIGTPYWMAPPEVVMCEETMKDTPYDYKADIWSLGITLIEMAQIEPPHHEL 240

*****
*****
Db 241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLQHPFVSRVTSN 300
Qy 241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLLEHPFVSSITSN 300

*****
*****
Db 301 KALRELVAEAKAEVMEEIEDGREDEGEEDAVDAVPPPLVNHTQDSANVTQPSLDSNKLQD 360
Qy 301 KALRELVAEAKAEVMEEIEDGREDEGEEDAVDAASTLENHTQNSSEVSPPSLNADKPLEE 360
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Fig. 15A



**Fig. 15C**